

Customized FORM PTO-1390 U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTORNEY DOCKET NO. P07180US00/BAS
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371		U.S. APPLICATION NO. <i>(if known see 37 CFR 1.5)</i> 097830433
INTERNATIONAL APPLICATION NO. PCT/FR99/02643	INTERNATIONAL FILING DATE 28 October 1999	PRIORITY DATE CLAIMED 30 October 1998
TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES SPECIFIC OF THE NEISSERIA GENUS...		
APPLICANT(S) FOR DO/EO/US: AUJAME et al.		
Applicant herewith submits to the US Designated/Elected Office (DO/EO/US) the following items and other information:		
<p><input checked="" type="checkbox"/> 1. This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.</p> <p><input type="checkbox"/> 2. This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 USC 371.</p> <p><input checked="" type="checkbox"/> 3. This express request to begin national examination procedures (35 USC 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 USC 371(b) and PCT Art. 22 and 39(1).</p> <p><input checked="" type="checkbox"/> 4. A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.</p> <p><input checked="" type="checkbox"/> 5. A copy of the International Application as filed (35 U.S.C. 371 (c)(2))</p> <p style="padding-left: 20px;"><input type="checkbox"/> a. is transmitted herewith (required only if not transmitted by the International Bureau).</p> <p style="padding-left: 20px;"><input checked="" type="checkbox"/> b. has been transmitted by the International Bureau.</p> <p style="padding-left: 20px;"><input type="checkbox"/> c. is not required, as the application was filed in the United States Receiving Office (RO/US).</p> <p><input checked="" type="checkbox"/> 6. A translation of the International Application into English (35 U.S.C. 371(c)(2)).</p> <p><input type="checkbox"/> 7. Amendments to the claims of the International Appln. under PCT Article 19 (35 USC 371 (c)(3))</p> <p style="padding-left: 20px;"><input type="checkbox"/> a. are transmitted herewith (required only if not transmitted by the International Bureau).</p> <p style="padding-left: 20px;"><input type="checkbox"/> b. have been transmitted by the International Bureau.</p> <p style="padding-left: 20px;"><input type="checkbox"/> c. have not been made; however, the time limit for making such amendments had NOT expired.</p> <p style="padding-left: 20px;"><input type="checkbox"/> d. have not been made and will not be made.</p> <p><input type="checkbox"/> 8. A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).</p> <p><input type="checkbox"/> 9. An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).</p> <p><input type="checkbox"/> 10. A translation of the annexes to the Int'l Prelim. Exam. Report under PCT Article 36 (35 U.S.C. 371(c)(5)).</p> <p>Items 11. to 20. below concern document(s) or information included:</p> <p><input type="checkbox"/> 11. An Information Disclosure Statement under 37 C.F.R. 1.97 and 1.98.</p> <p><input type="checkbox"/> 12. An Assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.</p> <p><input type="checkbox"/> 13. A First preliminary amendment.</p> <p><input type="checkbox"/> 14. A Second or Subsequent preliminary amendment.</p> <p><input type="checkbox"/> 15. A substitute specification.</p> <p><input type="checkbox"/> 16. A change of power of attorney and/or address letter.</p> <p><input type="checkbox"/> 17. A computer-readable form of the sequence listing in accordance with PCT Rule 13ter.2 & 35 USC 1.821-825.</p> <p><input type="checkbox"/> 18. A second copy of the published international application under 35 USC 154(d)(4).</p> <p><input type="checkbox"/> 19. A second copy of the English translation of the international application under 35 USC 154(d)(4).</p> <p><input type="checkbox"/> 20. Other items or information:</p> <p style="padding-left: 20px;"><input type="checkbox"/></p> <p style="padding-left: 20px;"><input type="checkbox"/></p> <p><input type="checkbox"/> A copy of the Notification of Missing Requirements under 35 U.S.C. 371.</p> <p><input type="checkbox"/> In the event that a petition for extension of time is required to be submitted herewith, and in the event that a separate petition does not accompany this response, applicant hereby petitions under 37 CFR 1.136(a) for an extension of time of as many months as are required to render this submission timely. Any fee is authorized in 17(c).</p>		
Date: April 26, 2001		

U.S. APPLICATION NO. <i>(if known)</i> 097 830433		INTERNATIONAL APPLICATION NO. PCT/FR99/02643		ATTORNEY DOCKET NO. P07180US00/BAS																																																							
X 21. The following fees are submitted: X Basic National Fee (37 CFR 1.492 (a) (1)-(5):				CALCULATIONS PTO USE ONLY																																																							
<input type="checkbox"/> Neither Int'l Prelim. Exam. fee nor Int'l Search fee paid to USPTO \$1000 <input checked="" type="checkbox"/> Search Report has been prepared by the EPO or JPO \$ 860 <input type="checkbox"/> No Int'l Prelim. Ex. fee paid to USPTO but Int'l Search fee paid to USPTO \$ 710 <input type="checkbox"/> International preliminary examination fee paid to USPTO \$ 690 <input type="checkbox"/> Int'l Prelim. Ex. fee paid to USPTO & all claims satisfied PCT Art. 33(1)-(4) \$ 100																																																											
ENTER APPROPRIATE BASIC FEE AMOUNT =						\$ 860.00																																																					
<input type="checkbox"/> Surcharge of \$130 for furnishing the oath or declaration later than from the earliest claimed priority date (37 CFR 1.492(e)).						<input type="checkbox"/> 20 mos. <input type="checkbox"/> 30 mos. +	\$																																																				
<table border="1"> <thead> <tr> <th>CLAIMS</th> <th>NUMBER FILED</th> <th>NUMBER EXTRA</th> <th>RATE</th> </tr> </thead> <tbody> <tr> <td>Total Claims</td> <td>- 20 =</td> <td></td> <td>X \$18 =</td> </tr> <tr> <td>Independent Claims</td> <td>- 03 =</td> <td></td> <td>X \$80 =</td> </tr> <tr> <td colspan="3"> <input type="checkbox"/> Multiple Dependent Claim(s) (if applicable) </td> <td>+ \$270 =</td> </tr> <tr> <td colspan="3"> TOTAL OF ABOVE CALCULATIONS = </td> <td>\$ 860.00</td> </tr> <tr> <td colspan="3"> <input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2. </td> <td>-</td> </tr> <tr> <td colspan="3"> SUBTOTAL = </td> <td>\$ 860.00</td> </tr> <tr> <td colspan="3"> <input type="checkbox"/> Processing fee of \$130 for furnishing the English translation later than from the earliest claimed priority date (37 CFR 1.492(f)). </td> <td> <input type="checkbox"/> 20 mos. <input type="checkbox"/> 30 mos. + </td> <td>\$</td> </tr> <tr> <td colspan="3"> TOTAL NATIONAL FEE = </td> <td>\$ 860.00</td> </tr> <tr> <td colspan="3"> <input type="checkbox"/> Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40 per property </td> <td>+</td> <td>\$</td> </tr> <tr> <td colspan="3"> TOTAL FEES ENCLOSED = </td> <td>\$ 860.00</td> </tr> <tr> <td colspan="3"> Amount to be </td> <td> Refunded </td> <td>\$</td> </tr> <tr> <td colspan="3"> Amount to be </td> <td> Charged </td> <td>\$</td> </tr> </tbody> </table>						CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE	Total Claims	- 20 =		X \$18 =	Independent Claims	- 03 =		X \$80 =	<input type="checkbox"/> Multiple Dependent Claim(s) (if applicable)			+ \$270 =	TOTAL OF ABOVE CALCULATIONS =			\$ 860.00	<input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.			-	SUBTOTAL =			\$ 860.00	<input type="checkbox"/> Processing fee of \$130 for furnishing the English translation later than from the earliest claimed priority date (37 CFR 1.492(f)).			<input type="checkbox"/> 20 mos. <input type="checkbox"/> 30 mos. +	\$	TOTAL NATIONAL FEE =			\$ 860.00	<input type="checkbox"/> Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40 per property			+	\$	TOTAL FEES ENCLOSED =			\$ 860.00	Amount to be			Refunded	\$	Amount to be		
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Amount to be			Charged	\$																																																							
X a. A check in the amount of \$ 860.00 to cover the above fees is enclosed. <input type="checkbox"/> b. Please charge my Deposit Account No. 12-0555 in the amount of \$ to cover the above fees. X c. The Commissioner is hereby authorized to charge any additional fees required or credit overpayment to Deposit Account No. 12-0555.																																																											
Note: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.																																																											
SEND ALL CORRESPONDENCE TO: B. Aaron Schulman At the address (below) of CUSTOMER NO. 00881. LARSON & TAYLOR, PLC 1199 NORTH FAIRFAX ST. SUITE 900 ALEXANDRIA, VA 22314			SIGNATURE: <i>Douglas E. Jackson</i> NAME: Douglas E. Jackson REG. NO.: 28,518 PHONE NO.: 703-739-4900 Date: April 26, 2001																																																								

409130 440E960

5

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re patent application of: AUJAME et al.

Serial No.: 09/830,433

Examiner:

Filed: April 26, 2001

Art Unit:

For: NUCLEIC ACID AND POLYPEPTIDES SPECIFIC
OF THE NEISSERIA GENUS...

Docket No.: P07180US00/BAS

PRELIMINARY AMENDMENT

Honorable Commissioner for Patents

Washington, DC 20231

S I R:

In response to the Notice dated December 6, 2001, please amend the
application as follows:

IN THE SPECIFICATION:

After Page 49, please substitute the attached Sequence Listing for any
Sequence Listing previously filed in the application.

REMARKS

By this Preliminary Amendment, Applicants are submitting a revised Sequence
Listing which overcomes the objections pointed out in the Notice dated December 6,
2001, as well as a copy of the paper sequence in computer readable form.

09/830,433

STATEMENT UNDER 37 CFR § 1.821

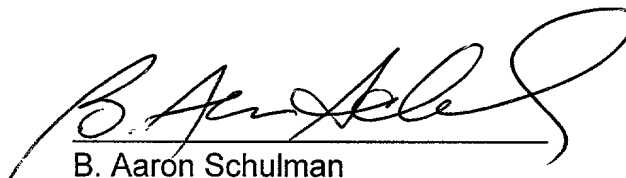
Applicants hereby certify in accordance with 37 C.F.R. 1.821(f) that the content of the enclosed paper sequence listing and computer readable form of the sequence listing are the same. In accordance with 37 C.F.R. 1.821(g), Applicants hereby certify that the enclosed submission contains no new matter.

In light of the foregoing, it is submitted that all prior objections have been overcome, and that the present application should be examined and passed on to allowance at the earliest possible time.

Respectfully submitted,

LARSON & TAYLOR, PLC

Date: February 5, 2002

A handwritten signature in black ink, appearing to read "B. Aaron Schulman", written over a horizontal line.

B. Aaron Schulman
Registration No. 31,877

Transpotomac Plaza
1199 N. Fairfax Street
Suite 900
Alexandria, VA 22314
(703) 739-4900

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Patent

In re patent application of: AUJAME et al.

Serial No.: 09/830,433

Examiner:

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Art Unit:

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OF THE NEISSERIA GENUS...

Docket No.:

P07180US00/BAS

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C.

S I R:

Prior to examination, please amend the above-identified application as follows.

IN THE SPECIFICATION:

After page 49, please insert the enclosed Sequence Listing as a substitute for the one filed in the original application.

IN THE CLAIMS:

A clean version of the amended claims is provided herewith in **Attachment A**. It will be noted that the claims have been amended relative to the previously provided version as shown by the marked up version thereof in **Attachment B** provided herewith.

REMARKS

By this Amendment, the claims have been rewritten to reduce the multiple dependencies. In addition, in response to the Notice to Comply with the sequence listing requirements, a computer readable form and paper copy of the Sequence Listing is now provided, and Applicants state that the paper copy and computer readable form are identical and add no new matter to the application.

RECEIVED 14 AUG 2001

Examination and allowance of the present application is thus earnestly solicited.

Respectfully submitted,

Date: 16 August 2001

By:



B. Aaron Schulman
Registration No. 31,877

LARSON & TAYLOR PLC
Transpotomac Plaza
1199 North Fairfax Street, Suite 900
Alexandria, Virginia 22314
(703) 739-4900

093049-040360

ATTACHMENT A

Clean Replacement/New Claims

Following herewith is a clean copy of each claim which replaces each previous claim having the same number and each new claim.

7. (Amended) Expression vector comprising an expression cassette in which a nucleotide sequence as defined in Claim 1 is placed under conditions allowing its expression in a host cell.

9. Canceled.

10. (Amended) Monospecific antibody directed against a polypeptide according to Claim 5.

11. (Amended) Use of a nucleic acid according to Claim 1, or of a polypeptide specific for pathogenic *Neisseria* strains or of antigenic fragments thereof, for manufacturing a pharmaceutical composition intended for vaccination against *Neisseria*.

12. (New) A pharmaceutical composition comprising a nucleic acid according to Claim 1, in naked form or in combination with at least one agent facilitating transfection, and optionally in combination with a pharmaceutically acceptable vehicle.

13. (New) A pharmaceutical composition comprising a vaccination vector comprising a nucleotide sequence according to Claim 1, such as in particular a virus or a bacterium, and optionally in combination with a pharmaceutically acceptable vehicle.

14. (New) A pharmaceutical composition comprising a polypeptide according to Claim 5, optionally in combination with a pharmaceutically acceptable vehicle.

ATTACHMENT B

Marked Up Replacement Claims

Following herewith is a marked up copy of each rewritten claim.

7. (Amended) Expression vector comprising an expression cassette in which a nucleotide sequence as defined in ~~one of Claims 1 to 4~~ Claim 1 is placed under conditions allowing its expression in a host cell.

9. Canceled.

10. (Amended) Monospecific antibody directed against a polypeptide according to ~~either of Claims 5 and 6~~ Claim 5.

11. (Amended) Use of a nucleic acid according to ~~one of Claims 1 to 4~~ Claim 1, or of a polypeptide specific for pathogenic *Neisseria* strains or of antigenic fragments thereof, ~~according to either of Claims 5 and 6~~, for manufacturing a pharmaceutical composition intended for vaccination against *Neisseria*.

12. (New) A pharmaceutical composition comprising a nucleic acid according to Claim 1, in naked form or in combination with at least one agent facilitating transfection, and optionally in combination with a pharmaceutically acceptable vehicle.

13. (New) A pharmaceutical composition comprising a vaccination vector comprising a nucleotide sequence according to Claim 1, such as in particular a virus or a bacterium, and optionally in combination with a pharmaceutically acceptable vehicle.

14. (New) A pharmaceutical composition comprising a polypeptide according to Claim 5, optionally in combination with a pharmaceutically acceptable vehicle.

SECRET

<120> Nucleic acids and polypeptides specific for pathogenic strains of the Neisseria genus

<140> 09/830,433

<141> 2001-04-26

<150> FR 98 13 693

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090443 0804

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096043.091501

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cgc Arg	aat Asn	aca Thr	atc Ile 340	cag Gln	gca Ala	ctc Leu	aca Thr	aaa Lys 345	tcc Ser	aat Asn	gca Ala	caa Gln	gaa Glu 350	act Thr	gac Asp	1056
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 Leu His Lys Met Leu Pro Ile Ser Leu Val Gln Ser Leu Leu Arg Phe
 35 40 45
 Gly Glu Arg Val His Leu Val Gln Leu Gln Lys Thr Gly Lys Asn Ala
 50 55 60
 Leu Asp Phe Tyr Leu Ser Tyr Tyr Leu Gly Gln Ile Thr Ala Thr Asp
 65 70 75 80
 Pro Asn Ala Gln Ile Gly Ile Leu Ser Arg Asp Gly Gly Tyr Asp Val
 85 90 95
 Leu Val Glu His Ile Leu Lys Asn His Gln Ala Lys Gly Ile Val Arg
 100 105 110
 Leu Ala Asn Ile Asp Glu Val Gln His Gln Lys Ile Ala Thr Glu Pro
 115 120 125
 Pro Ser Ala Leu Leu Glu Asn Thr Pro Gln Pro Glu Thr Thr Leu Lys
 130 135 140
 Pro Gln Gln Pro Leu Thr Ser Tyr Phe Gln Ala Ala Leu Thr Ala Leu
 145 150 155 160
 Arg Arg Pro Asp Ala Phe Arg Pro Cys Arg Leu His Asn Leu Arg Gln
 165 170 175
 Asn Leu Arg Lys His Ile Leu Ser Asp Leu Phe Lys Glu Lys Thr Asp
 180 185 190
 Glu Glu Cys Glu Ile Thr Thr Ala Asn Val Ile Asn Lys Leu Lys Ala
 195 200 205
 Gln Asn Phe Ile Ser Ile Asp Glu Gln Glu Thr Val Ser Tyr His Leu
 210 215 220
 Ser Asp Asn Asp Leu Leu Gln Arg Ile Gln Arg His Ile Leu Ser Gln
 225 230 235 240
 Arg Pro Lys Thr Tyr Ala Asp Phe Gln Ala Val Val Gln Asn Arg Ala
 245 250 255
 Asp Ala Leu His Leu Thr Val Gly Thr Asn Asp Ile Gln Ser Phe Ala
 260 265 270
 Arg His Leu Arg Asp Gln Asn Leu Ile Arg Gln Asn Asn Gly Lys Ile
 275 280 285
 Glu Tyr Ala Pro Phe Thr Glu Pro Lys Pro Gln Pro Thr Pro Lys Gln
 290 295 300

093043-081504

Pro Lys Lys Thr Ala Trp Glu Pro Asp Glu Ile Ile Trp Lys Lys Val
 305 310 315 320

Ile Ala Ala Leu Ser Leu Lys Asn Arg Pro Asn Lys Thr Lys Thr Leu
 325 330 335

Arg Asn Thr Ile Gln Ala Leu Thr Lys Ser Asn Ala Gln Glu Thr Asp
 340 345 350

Lys Leu Leu Gln His Leu Gln Asp Asp Pro Ser Pro Thr Tyr
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gcc agc gaa atc gcc tat cgc ttt gta ttc gga att gaa acc tta ccg 96
 Ala Ser Glu Ile Ala Tyr Arg Phe Val Phe Gly Ile Glu Thr Leu Pro
 20 25 30

gct gca aaa atg gca gaa acg ttt gcg ctg aca ttt atg att gct gcg 144
 Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala
 35 40 45

ctg tat ctg ttt gcg cgt tat aag gct tcg cgg ctg ctg att gcg gtg 192
 Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val
 50 55 60

ttt ttc gcg ttc agc att att gcc aac aat gta cat tat gcg gtt tat 240
 Phe Phe Ala Phe Ser Ile Ile Ala Asn Asn Val His Tyr Ala Val Tyr
 65 70 75 80

caa agt tgg atg acg ggc atc aat tat tgg ctg atg ctg aaa gag att 288
 Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Ile
 85 90 95

acc gaa gtc ggc agt gcg ggc gcg tcg atg ttg gat aag ttg tgg ctg 336
 Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu
 100 105 110

cct gcg ttg tgg ggc gtg ttg gaa gtc atg ttg ttt tgc agc ctt gcc 384
 Pro Ala Leu Trp Gly Val Leu Glu Val Met Leu Phe Cys Ser Leu Ala
 115 120 125

aag ttc cac cgt aag acg cat ttt tct gcc gat ata ctg ttt gcc ttc 432
 Lys Phe His Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe
 130 135 140

cta atg ctg atg att ttc gtg cgt tcg ttc gac acg aaa caa gag cac 480
 Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His
 145 150 155 160

ggt att tcg ccc aaa ccg aca tac agc cgc atc aaa gcc aat tat ttc 528

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Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe
 165 170 175

agc ttc ggt tat ttt gtc gga cgc gtg ttg ccg tat cag ttg ttt gat 576
 Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp
 180 185 190

tta agc agg att ccc gcc ttt aag cag cct gct cca agc aaa atc ggg 624
 Leu Ser Arg Ile Pro Ala Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly
 195 200 205

cag ggc agt gtt caa aat atc gtc ctg att atg ggc gaa agc gaa agc 672
 Gln Gly Ser Val Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser
 210 215 220

gcg gcg cat ttg aag ctg ttt ggc tac gga cgc gaa act tcg ccg ttt 720
 Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe
 225 230 235 240

tta acc cgg ctg tcg caa gcc gat ttt aag ccg att gtg aaa caa agt 768
 Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser
 245 250 255

tat tcc gca ggc ttt atg act gca gtg tcc ctg ccc agt ttt ttc aat 816
 Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn
 260 265 270

gcg ata ccg cac gcc aac ggc ttg gaa caa atc agc ggc ggc gat act 864
 Ala Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr
 275 280 285

aat atg ttc cgc ctc gcc aaa gag cag ggc tat gaa acg tat ttt tac 912
 Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr
 290 295 300

agc gca cag gcg gaa aac gag atg gcg att ttg aac tta atc ggt aag 960
 Ser Ala Gln Ala Glu Asn Glu Met Ala Ile Leu Asn Leu Ile Gly Lys
 305 310 315 320

aaa tgg ata gac cat ctg att cag ccg acg cag ctt ggc tac ggc aac 1008
 Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn
 325 330 335

ggc gac aat atg ccc gat gag aag ctg ctg ccg ctg ttc gac aaa atc 1056
 Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile
 340 345 350

aat ttg cag cag ggc agg cat ttt atc gtg ttg cac caa cgt ggt tcg 1104
 Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser
 355 360 365

cac gcc cca tac agc gca ttg ttg cag cct caa gat aaa gta ttc ggc 1152
 His Ala Pro Tyr Ser Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly
 370 375 380

gaa ctt att gtg gat aag tac gac aac acc atc cac aaa acc gac caa 1200
 Glu Leu Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp Gln
 385 390 395 400

atg att caa acc gta ttc gag cag ctg caa aag cag cct gac ggc aac 1248
 Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly Asn
 405 410 415

tgg ctg ttt gcc tat acc tcc gat cat ggc cag tat gtt cgc caa gat 1296
 Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln Asp
 420 425 430

09830433.081601

atc tac aat caa ggc acg gtg cag ccc gac agc tat ctc gtg ccg ctg	1344
Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Leu Val Pro Leu	
435 440 445	
gtg ttg tac agc tcg aat aag gcc gtg caa cag gct gcc aac cag gct	1392
Val Leu Tyr Ser Ser Asn Lys Ala Val Gln Gln Ala Ala Asn Gln Ala	
450 455 460	
ttt gcg cct tgc gag att gcc ttc cat cag cag ctt tca acg ttc ctg	1440
Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe Leu	
465 470 475 480	
att cac acg ttg ggc tac gat atg ccg gtt tca ggt tgt cgc gaa ggc	1488
Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu Gly	
485 490 495	
tcg gta acg ggc aac ctg att acg ggt gat gca gcc agc ttg aac att	1536
Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn Ile	
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Arg Asp Gly Lys Ala Glu Tyr Val Tyr Pro Gln	
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 35 40 45
 Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val
 50 55 60
 Phe Phe Ala Phe Ser Ile Ile Ala Asn Asn Val His Tyr Ala Val Tyr
 65 70 75 80
 Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Ile
 85 90 95
 Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu
 100 105 110
 Pro Ala Leu Trp Gly Val Leu Glu Val Met Leu Phe Cys Ser Leu Ala
 115 120 125
 Lys Phe His Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe
 130 135 140
 Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His
 145 150 155 160
 Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe
 165 170 175
 Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp

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 Met Ala Leu Ala Val Ala Thr Thr Leu Ser Ala Cys Leu Gly Gly Gly
 20 25 30

ggc ggc act tct gcg ccc gac ttc aat gca ggc ggc acc ggt atc ggc 144
 Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly
 35 40 45

agc aac agc aga gca aca aca gcg aaa tca gca gca gta tct tac gcc 192
 Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala
 50 55 60

ggt atc aag aac gaa atg tgc aaa gac aga agc atg ctc tgt gcc ggt 240
 Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly
 65 70 75 80

cgg gat gac gtt gcg gtt aca gac agg gat gcc aaa atc aat gcc ccc 288
 Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro
 85 90 95

ccc ccg aat ctg cat acc gga gac ttt aca aac cca aat gac gca tac 336
 Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn Pro Asn Asp Ala Tyr
 100 105 110

aag aat ttg atc aac ctc aaa cct gca att gaa gca ggc tat aca gga 384
 Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly
 115 120 125

cgc ggc gta gag gta ggt atc gtc gat aca ggc gaa tcc gtc ggc agc 432
 Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser
 130 135 140

ata tcc ttt ccc gaa ctg tat ggc aga aaa gaa cac ggc tat aac gaa 480
 Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu
 145 150 155 160

aat tac aaa aac tat acg gcg tat atg cgg aag gaa gcg cct gaa gac 528
 Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp
 165 170 175

gga ggc ggt aaa gac att aaa gct tct ttc gac gat gag gcc gtt ata 576
 Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp Asp Glu Ala Val Ile
 180 185 190

gag act gaa gca aag ccg acg gat atc cgc cac gta aaa gaa atc gga 624
 Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly
 195 200 205

cac atc gat gtg gtc tcc cat att att ggc ggc cgt tcc gtg gac ggc 672
 His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly
 210 215 220

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gcc gct acc gtc tat gcc gac agt acc gcc gcc cat gcc gat atg cag Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln 770 775 780	2352
gga cgc cgg ctg aaa gcc gta tcg gac ggg ttg gac cac aac gct acg Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Ala Thr 785 790 795 800	2400
ggg ctg cgc gtc atc gcg caa acc caa cag gac ggt gga acg tgg gaa Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu 805 810 815	2448
cag ggc ggt gtt gaa ggc aaa atg cgc ggc agt acc caa acc gtc ggc Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly 820 825 830	2496
att gcc gcg aaa acc ggc gaa aat acg aca gca gcc gcc aca ctg ggc Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly 835 840 845	2544
atg gga cac agc aca tgg agc gaa aac agt gca aat gca aaa acc gac Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp 850 855 860	2592
agc att agt ctg ttt gca ggc ata cgg cac gat gcg ggc gat atc ggc Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly 865 870 875 880	2640
tat ctc aaa ggc ctg ttc tcc tac gga cgc tac aaa aac agc atc agc Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser 885 890 895	2688
cgc agc acc ggt gcg gac gaa cat gcg gaa ggc agc gtc aac ggc acg Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr 900 905 910	2736
ctg atg cag ctg ggc gca ctg ggc ggt gtc aac gtt ccg ttt gcc gca Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala 915 920 925	2784
acg gga gat ttg acg gtc gaa ggc ggt ctg cgc tac gac ctg ctc aaa Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys 930 935 940	2832
cag gat gca ttc gcc gaa aaa ggc agt gct ttg ggc tgg agc ggc aac Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn 945 950 955 960	2880
agc ctc act gaa ggc aca ctg gtc gga ctc gcg ggt ctg aag ctg tcg Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser 965 970 975	2928
caa ccc ttg agc gat aaa gcc gtc ctg ttt gca acg gcg ggc gtg gaa Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu 980 985 990	2976
cgc gac ctg aac gga cgc gac tac acg gta acg ggc ggc ttt acc ggc Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly 995 1000 1005	3024
gcg act gca gca acc ggc aag acg ggg gca cgc aat atg ccg cac acc	3072

Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr
1010 . . 1015 1020

cgc ctg gtt gcc ggt ctg ggc gcg gat gtc gaa ttc ggc aac ggc tgg 3120
Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp
1025 1030 1035 1040

aac ggc ttg gca cgt tac agc tac gcc ggt tcc aaa cag tac ggc aac 3168
Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn
1045 1050 1055

cac agc gga cga gtc ggc gta ggc tac cgg ttc tga 3204
His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe
1060 1065

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Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly
35 40 45

Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala
50 55 60

Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly
65 70 75 80

Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro
85 90 95

Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn Pro Asn Asp Ala Tyr
100 105 110

Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly
115 120 125

Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser
130 135 140

Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu
145 150 155 160

Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp
165 170 175

Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp Asp Glu Ala Val Ile
180 185 190

Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly
195 200 205

His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly
210 215 220

Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn
225 230 235 240

094043 094043

Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser Ala Ala Ile Arg Asn
 245 250 255
 Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser
 260 265 270
 Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp His Phe Gln Ile Ala
 275 280 285
 Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Ala Tyr Ser Gly Gly
 290 295 300
 Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly
 305 310 315 320
 Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser
 325 330 335
 Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr Leu Thr Leu Leu Pro
 340 345 350
 Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val
 355 360 365
 Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn His Cys Gly Ile Thr
 370 375 380
 Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr
 385 390 395 400
 Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile
 405 410 415
 Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser
 420 425 430
 Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr Ala Gln Asp Ile Gly
 435 440 445
 Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly Leu Leu Asp Ala Gly
 450 455 460
 Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala
 465 470 475 480
 Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile
 485 490 495
 Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu
 500 505 510
 His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser
 515 520 525
 Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys
 530 535 540
 Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly Gly Ser Leu Asn Ser
 545 550 555 560
 Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg Ser Gly Ala Asn Glu
 565 570 575
 Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly Gly Glu Gly Thr Leu
 580 585 590

109130 6640360

Tyr Thr Arg Leu Gly Lys Leu Leu Lys Val Asp Gly Thr Ala Met Thr
 595 600 605
 Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys Gly Ala Gly Tyr Leu
 610 615 620
 Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser Ala Ala Lys Ile Gly
 625 630 635 640
 Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu
 645 650 655
 Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly Ser Glu Gly Asp Thr
 660 665 670
 Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala Arg Thr Ala Ser Ala
 675 680 685
 Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly
 690 695 700
 Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu Asp Ala Ser Glu Ser
 705 710 715 720
 Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp
 725 730 735
 Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala
 740 745 750
 Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu
 755 760 765
 Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln
 770 775 780
 Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Ala Thr
 785 790 795 800
 Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu
 805 810 815
 Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly
 820 825 830
 Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly
 835 840 845
 Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp
 850 855 860
 Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly
 865 870 875 880
 Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser
 885 890 895
 Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr
 900 905 910
 Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala
 915 920 925
 Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys
 930 935 940

093043 "093043"

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Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser
 965 970 975

Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu
 980 985 990

Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly
 995 1000 1005

Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr
 1010 1015 1020

Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp
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Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn
 1045 1050 1055

His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe
 1060 1065

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 <213> Neisseria meningitidis

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gca ggt tgc ggc tca atc aat aat gta acc gtt tcc gac cag aaa ctt 96
 Ala Gly Cys Gly Ser Ile Asn Asn Val Thr Val Ser Asp Gln Lys Leu
 20 25 30

cag gaa cgt gcc gcg ttt gcc ttg ggc gtc agc caa aat gcc gta aaa 144
 Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys
 35 40 45

atc agc aac cgc agc aat gaa agc ata cgc atc aac ttt acc gca act 192
 Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr
 50 55 60

gtg ggt aag cgc gtg agc caa tgc tat gtt acc agt gta atc agc aca 240
 Val Gly Lys Arg Val Ser Gln Cys Tyr Val Thr Ser Val Ile Ser Thr
 65 70 75 80

atc ggc gtt acc act tcc gat gca att tgt ttg gga ggc gga acg cac 288
 Ile Gly Val Thr Thr Ser Asp Ala Ile Cys Leu Gly Gly Gly Thr His
 85 90 95

aaa ggc aaa agt caa tgc aat gct ttg ctt aaa gcg gca ggc cgt tgc 336
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 100 105 110

taa 339

09403-09403

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Met	Leu	Thr	Phe	Ile	Gly	Leu	Leu	Ile	Ile	Gly	Val	Ile	Val	Trp	Leu		
1			5			10			15								
ctg	ctg	acg	gaa	aaa	gtg	tcg	ccc	atc	atc	gca	tta	atc	ttg	gtg	ccg	96	
Leu	Leu	Thr	Glu	Lys	Val	Ser	Pro	Ile	Ile	Ala	Leu	Ile	Leu	Val	Pro		
			20			25			30								
ctg	ttt	ggg	gcg	ttg	ctg	gcg	ggg	ttt	gat	gta	tcc	caa	tta	aaa	gaa	144	
Leu	Phe	Gly	Ala	Leu	Leu	Ala	Gly	Phe	Asp	Val	Ser	Gln	Leu	Lys	Glu		
			35			40			45								
ttt	tat	tcg	ggc	ggc	acc	aaa	tcg	gtg	atg	cag	att	gtg	att	atg	ttt	192	
Phe	Tyr	Ser	Gly	Gly	Thr	Lys	Ser	Val	Met	Gln	Ile	Val	Ile	Met	Phe		
50						55			60								
atg	ttt	tcc	att	ttg	ttt	ttt	gga	atc	atg	aac	gat	gtg	ggg	ctg	ttc	240	
Met	Phe	Ser	Ile	Leu	Phe	Phe	Gly	Ile	Met	Asn	Asp	Val	Gly	Leu	Phe		
65			70			75			80								
cgt	ccg	atg	ata	ggc	ggt	ttg	att	aag	ctg	act	cgg	ggt	aat	atc	gtg	288	
Arg	Pro	Met	Ile	Gly	Gly	Leu	Ile	Lys	Leu	Thr	Arg	Gly	Asn	Ile	Val		
			85			90			95								
gca	gtg	agt	gtg	ggg	acg	gtc	ttg	gtg	tcg	gtg	gtg	gcg	cag	ttg	gac	336	

Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp
 100 . 105 110

ggg gcg ggt gcg acg acg ttt tta ttg gtc gtc ccc gcc ctt ttg ccg 384
 Gly Ala Gly Ala Thr Thr Phe Leu Leu Val Val Pro Ala Leu Leu Pro
 115 120 125

ctt tac aag cgt ctg cat atg aat cct tac ctg ctg ttt ttg ctg ctg 432
 Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu
 130 135 140

act tcc agt gcg gga ttg att aac ctt ctg ccg tgg ggc ggg ccg acc 480
 Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Trp Gly Gly Pro Thr
 145 150 155 160

ggg cgg gtt gca agc gtg ttg ggc gca gat gtg ggc gaa ttg tat aaa 528
 Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys
 165 170 175

cct ttg ttg acg gtg caa att atc ggt gtg gtg ttt atc ctt gcg ctg 576
 Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Ala Leu
 180 185 190

tcc ctg ctt ttg ggt gtg cgt gaa aaa agg ccg att gtc ccg gag ttg 624
 Ser Leu Leu Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu
 195 200 205

ggc gcg ttg ccc gcc gtg gcg gat ttg ata aag ccg gtg cct ttg tcg 672
 Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Val Pro Leu Ser
 210 215 220

gaa gaa gaa caa aaa ttg gcg cgt ccg aaa ctg ttt tgg tgg aat gtc 720
 Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val
 225 230 235 240

ctg ctg ttt ttg gcg gcg atg agc ctg ctt ttt tcg ggc atc ttc ccg 768
 Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro
 245 250 255

ccg ggt tat gta ttt atg ctg gct gca acg gcg gcg ttg ctt ttg aat 816
 Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Asn
 260 265 270

tac cgc agc ccg cag gaa cag atg gag ccg att tat gcc cac gcc ggc 864
 Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly
 275 280 285

ggc gcg gtg atg atg gcg tcc att att ttg gcg gca ggt acg ttt ttg 912
 Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu
 290 295 300

ggg att ttg aag ggt gcg ggg atg ttg gac gcg att tcc aaa gac att 960
 Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Ile
 305 310 315 320

gtg cat atc ctg ccg gac gcg ctg ctg cct tat ctg cat att gcc atc 1008
 Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile
 325 330 335

ggt gtg ttg ggc att ccg ctt gag ttg gtt ttg agt acg gac gct tat 1056
 Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr
 340 345 350

tat ttc gga ctg ttt ccg att gtg gag cag att acc tcg cag gcg ggc 1104
 Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly
 355 360 365

109180" E40E360

gtg gcg ccc gaa gca. gca ggt tat gcg atg ttg atc ggc agt atc gtc 1152
Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val
370 375 380

ggc act ttt gtt acg ccg ctt tcg ccg gct ttg tgg atg ggc ttg ggt 1200
Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly
385 390 395 400

ttg gcg aaa ttg tcg atg ggc aaa cac atc cgt tat tcg ttt ttt tgg 1248
Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp
405 410 415

gcg tgg ggt ttg tcg ctg gcg ata ttg gcc agt tcg ata gcg gca gga 1296
Ala Trp Gly Leu Ser Leu Ala Ile Leu Ala Ser Ser Ile Ala Ala Gly
420 425 430

atc gtg cct ctg ccg taa 1314
Ile Val Pro Leu Pro
435

<210> 12
<211> 437
<212> PRT
<213> Neisseria meningitidis

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Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro
20 25 30

Leu Phe Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu
35 40 45

Phe Tyr Ser Gly Gly Thr Lys Ser Val Met Gln Ile Val Ile Met Phe
50 55 60

Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe
65 70 75 80

Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val
85 90 95

Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp
100 105 110

Gly Ala Gly Ala Thr Thr Phe Leu Leu Val Val Pro Ala Leu Leu Pro
115 120 125

Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu
130 135 140

Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Trp Gly Gly Pro Thr
145 150 155 160

Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys
165 170 175

Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Ala Leu
180 185 190

Ser Leu Leu Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu
195 200 205

009430#EE40E360

Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Val Pro Leu Ser
 210 215 220
 Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val
 225 230 235 240
 Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro
 245 250 255
 Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn
 260 265 270
 Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly
 275 280 285
 Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu
 290 295 300
 Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Ile
 305 310 315 320
 Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile
 325 330 335
 Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr
 340 345 350
 Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly
 355 360 365
 Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val
 370 375 380
 Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly
 385 390 395 400
 Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp
 405 410 415
 Ala Trp Gly Leu Ser Leu Ala Ile Leu Ala Ser Ser Ile Ala Ala Gly
 420 425 430
 Ile Val Pro Leu Pro
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<210> 13
 <211> 1155
 <212> DNA
 <213> Neisseria meningitidis

<220>
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 <222> (1)..(1152)

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 act tat ctg tat caa aag ccc aag ctc ttt aaa gga gcg gtt cgg aat 96
 Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn
 20 25 30

009730.E40E350

ctc gaa gcc gca tct tgt aaa tat atc aac gag ata tac caa cga gca Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala	144
35 40 45	
gac cca acc gca ccg ctg ttt cat ctg cgt aaa aaa ggc gca atc gtt Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val	192
50 55 60	
cct aaa gaa gaa tac gtc gaa agt ttc gac gat ttg ggc aaa act cgc Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg	240
65 70 75 80	
tac cgt ttt att aaa tcc gtt atc tac gaa cat atg aag aat ggt gcg Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala	288
85 90 95	
tcg tta gtc tat aac cat att aac aac gag ccg ttt tca gac cat atc Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile	336
100 105 110	
gcc cgt caa gtc gcc cgc ttt gcc ggc gca cat act att gtt agt gga Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly	384
115 120 125	
tat ctt gct ttt ggc agc gac gaa tct tat aaa aac cat tgg gat acc Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr	432
130 135 140	
cgc gat gtg tat gcc atc cag ctt ttc ggc aag aaa cgt tgg caa ctt Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu	480
145 150 155 160	
act gcc cct gat ttc cct atg cca ttg tat atg caa cag act aaa gat Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp	528
165 170 175	
act gat att tcc att cct gaa cat atc gat atg gat att atc ctt gaa Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu	576
180 185 190	
gca ggt gat gtc ctc tac atc cca cgc ggt tgg tgg cac aga cct atc Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile	624
195 200 205	
ccg ctc ggc tgt gaa acc ttc cac ttc gct gtc ggt acc ttc ccg ccc Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro	672
210 215 220	
aac ggc tat aat tac ctc gag tgg cta atg aag aaa ttc ccc acg ata Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile	720
225 230 235 240	
gaa agt ctg cgc cac agt ttc tca gac tgg gag caa gat agg acg cgt Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg	768
245 250 255	
atc aac gat act gcc gca caa att gct gcc atg att gcc gac ccc gtc Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val	816
260 265 270	
aat tac gaa gcc ttc agt gaa gac ttc ctc ggc aaa gaa cgc acc gat Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp	864
275 280 285	
acc gct ttt cat ctc gaa cag ttc gcg aat ccc aac gct act ccg ctt Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu	912

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290

295

300

tca gac gac gtc agg ttg aga cta aat gcc aat aat ttg gat acg ttg 960
 Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu
 305 310 315 320

gaa aag gga tat ttg att ggg aat ggg atg aag ata agc gta gat gaa 1008
 Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu
 325 330 335

ttg ggg aaa aaa gtg tta gaa cac atc ggt aag aat gaa ccg tta ttg 1056
 Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu
 340 345 350

ttg aaa aat cta ctg gtt aac ttc aat cag gga aaa cat gaa gaa gtt 1104
 Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Gly Lys His Glu Glu Val
 355 360 365

agg aag ttg att tat cag ttg ata gag tta gat ttt ctg gaa ctt ttg 1152
 Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Leu Leu
 370 375 380

tga 1155

<210> 14

<211> 384

<212> PRT

<213> Neisseria meningitidis

<400> 14

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Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn
 20 25 30

Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala
 35 40 45

Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val
 50 55 60

Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg
 65 70 75 80

Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala
 85 90 95

Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile
 100 105 110

Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly
 115 120 125

Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr
 130 135 140

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu
 145 150 155 160

Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp
 165 170 175

Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu
 180 185 190

09130-0340360

Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp
 100 105 110

Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu
 115 120 125

Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr
 130 135 140

Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Lys Leu His
 145 150 155 160

Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu
 165 170 175

Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro
 180 185 190

Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala
 195 200 205

Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile
 210 215 220

Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala
 225 230 235

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 <211> 690
 <212> DNA
 <213> Neisseria meningitidis

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 <222> (1)..(687)

<400> 17
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 Met Met Asn Val Glu Ala Glu Leu Leu Glu Gln Lys Ala Lys Leu Asp
 1 5 10 15

gcc tac ggc cga gaa gaa gcc ggg ctg ctt cag gaa atc cgc acg cag 96
 Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln
 20 25 30

aat ctg aca ttg gcc agc ctc ccc aaa cgg cat gag aca gaa caa agc 144
 Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
 35 40 45

cag ctt gaa cgc acc atg gcc gat att tct caa gaa gtt ttg gat ttt 192
 Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
 50 55 60

gaa atg cgc tct gaa caa atc atc cgt gca gga cgg tcc ggt tat ata 240
 Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
 65 70 75 80

gca ata ccg aac gtc gaa gtc gga cag cag gtt gat cct tcc aaa ctg 288
 Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu
 85 90 95

ctc ttg agc att gtt ccc gaa cgt acc gag cta tat gcc cat cta tat 336

Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
 130 . . 135 140
 Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
 145 150 155 160
 Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
 165 170 175
 Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
 180 185 190
 Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
 195 200 205
 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser
 210 215 220
 Met Ser Gly Lys Leu
 225

<210> 19
 <211> 1743
 <212> DNA
 <213> Neisseria meningitidis

<220>
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 <222> (1)..(1740)

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 Met Lys Phe Phe Pro Ala Pro Cys Leu Leu Val Ile Leu Ala Val Ile
 1 5 10 15
 ccc ctt aaa acc tta gct gcc gat gaa aac gat gca gaa ctt atc cgt 96
 Pro Leu Lys Thr Leu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg
 20 25 30
 tcc atg cag cgt cag cag cac ata gat gct gaa ttg tta act gat gca 144
 Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala
 35 40 45
 aat gtc cgt ttc gag caa cca ttg gag aag aac aat tat gtc ctg agt 192
 Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser
 50 55 60
 gaa gat gaa aca ccg tgt act cgg gta aat tac att agt tta gat gat 240
 Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp
 65 70 75 80
 aag acg gcg cgc aaa ttt tct ttt ctt cct tct gtg ctc atg aaa gaa 288
 Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu
 85 90 95
 aca gct ttt aaa act ggg atg tgt tta ggt tcc aat aat ttg agc agg 336
 Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg
 100 105 110
 cta caa aaa gcc gcg caa cag ata ctg att gtg cgt ggc tac ctc act 384
 Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr
 115 120 125
 tcc caa gct att atc caa cca cag aat atg gat tcg gga att ctg aaa 432

109130-EE40E350

Ser	Gln	Ala	Ile	Ile	Gln	Pro	Gln	Asn	Met	Asp	Ser	Gly	Ile	Leu	Lys		
130						135					140						
tta	cgg	gta	tca	gca	ggc	gaa	atc	agg	gat	atc	cgc	tat	gaa	gaa	aaa	480	
Leu	Arg	Val	Ser	Ala	Gly	Glu	Ile	Arg	Asp	Ile	Arg	Tyr	Glu	Glu	Lys		
145					150					155					160		
cgg	gat	gcg	aag	tct	gcc	gag	ggc	agt	att	agt	gca	ttc	aat	aac	aaa	528	
Arg	Asp	Ala	Lys	Ser	Ala	Glu	Gly	Ser	Ile	Ser	Ala	Phe	Asn	Asn	Lys		
				165					170					175			
ctt	ccc	tta	tat	agg	aac	aaa	att	ctc	aat	ctt	cgc	gat	gta	gag	cag	576	
Leu	Pro	Leu	Tyr	Arg	Asn	Lys	Ile	Leu	Asn	Leu	Arg	Asp	Val	Glu	Gln		
			180					185					190				
ggc	ttg	gaa	aac	ctg	cgt	cgt	ttg	ccg	agt	gtt	aaa	aca	gat	att	cag	624	
Gly	Leu	Glu	Asn	Leu	Arg	Arg	Leu	Pro	Ser	Val	Lys	Thr	Asp	Ile	Gln		
		195					200					205					
att	ata	ccg	tcc	gaa	gaa	gaa	ggc	aaa	agc	gat	tta	cag	atc	aaa	tgg	672	
Ile	Ile	Pro	Ser	Glu	Glu	Glu	Gly	Lys	Ser	Asp	Leu	Gln	Ile	Lys	Trp		
	210					215					220						
cag	cag	aat	aaa	ccc	ata	cgg	ttc	agt	atc	ggt	ata	gat	gat	gcg	ggc	720	
Gln	Gln	Asn	Lys	Pro	Ile	Arg	Phe	Ser	Ile	Gly	Ile	Asp	Asp	Ala	Gly		
225					230					235					240		
ggc	aaa	acg	acc	ggc	aaa	tat	caa	gga	aat	gtc	gct	tta	tcg	tcc	gat	768	
Gly	Lys	Thr	Thr	Gly	Lys	Tyr	Gln	Gly	Asn	Val	Ala	Leu	Ser	Ser	Asp		
				245					250					255			
aac	cct	ttg	ggc	tta	agc	gat	tcg	ttt	tat	gtt	tca	tat	gga	cgc	ggt	816	
Asn	Pro	Leu	Gly	Leu	Ser	Asp	Ser	Phe	Tyr	Val	Ser	Tyr	Gly	Arg	Gly		
			260					265					270				
ttg	gtg	cac	aaa	acg	gac	ttg	act	gct	gcc	acc	ggt	acg	gaa	act	gaa	864	
Leu	Val	His	Lys	Thr	Asp	Leu	Thr	Ala	Ala	Thr	Gly	Thr	Glu	Thr	Glu		
		275					280					285					
agc	gga	tcc	aga	agt	tac	agc	gtg	cat	tat	tcg	gtg	ccc	gta	aaa	aaa	912	
Ser	Gly	Ser	Arg	Ser	Tyr	Ser	Val	His	Tyr	Ser	Val	Pro	Val	Lys	Lys		
	290					295					300						
tgg	ctg	ttt	tct	ttt	aat	cac	aat	gga	cat	cgt	tac	cac	gaa	gca	acc	960	
Trp	Leu	Phe	Ser	Phe	Asn	His	Asn	Gly	His	Arg	Tyr	His	Glu	Ala	Thr		
305					310					315					320		
gaa	ggc	tat	tcc	gtc	aat	tac	gat	tac	aac	ggc	aaa	caa	tat	cag	agc	1008	
Glu	Gly	Tyr	Ser	Val	Asn	Tyr	Asp	Tyr	Asn	Gly	Lys	Gln	Tyr	Gln	Ser		
				325					330					335			
agc	ctg	gcc	gcc	gag	cgc	atg	ctt	tgg	ccc	ccc	agc	ttt	cct	caa	act	1056	
Ser	Leu	Ala	Ala	Glu	Arg	Met	Leu	Trp	Pro	Pro	Ser	Phe	Pro	Gln	Thr		
			340					345					350				
tca	gtc	cga	atg	aaa	tta	tgg	aca	cgc	caa	acc	tat	aaa	tac	atc	gac	1104	
Ser	Val	Arg	Met	Lys	Leu	Trp	Thr	Arg	Gln	Thr	Tyr	Lys	Tyr	Ile	Asp		
		355					360					365					
gat	gcc	gaa	atc	gaa	gtg	caa	cgc	cgc	cgc	tct	gca	ggc	tgg	gaa	gcc	1152	
Asp	Ala	Glu	Ile	Glu	Val	Gln	Arg	Arg	Arg	Ser	Ala	Gly	Trp	Glu	Ala		
		370				375					380						
gaa	ttg	cgc	cac	cgt	gct	tac	ctc	cac	cgt	tgg	cag	ctt	gac	ggc	aag	1200	
Glu	Leu	Arg	His	Arg	Ala	Tyr	Leu	His	Arg	Trp	Gln	Leu	Asp	Gly	Lys		
385					390					395					400		

0983043 * 081604

093043-031601

50					55					60					
Glu	Asp	Glu	Thr	Pro	Cys	Thr	Arg	Val	Asn	Tyr	Ile	Ser	Leu	Asp	Asp
65					70					75					80
Lys	Thr	Ala	Arg	Lys	Phe	Ser	Phe	Leu	Pro	Ser	Val	Leu	Met	Lys	Glu
				85					90					95	
Thr	Ala	Phe	Lys	Thr	Gly	Met	Cys	Leu	Gly	Ser	Asn	Asn	Leu	Ser	Arg
			100					105					110		
Leu	Gln	Lys	Ala	Ala	Gln	Gln	Ile	Leu	Ile	Val	Arg	Gly	Tyr	Leu	Thr
		115					120					125			
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Arg	Asp	Ala	Lys	Ser	Ala	Glu	Gly	Ser	Ile	Ser	Ala	Phe	Asn	Asn	Lys
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Asn	Pro	Leu	Gly	Leu	Ser	Asp	Ser	Phe	Tyr	Val	Ser	Tyr	Gly	Arg	Gly
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Glu	Gly	Tyr	Ser	Val	Asn	Tyr	Asp	Tyr	Asn	Gly	Lys	Gln	Tyr	Gln	Ser
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Ser	Val	Arg	Met	Lys	Leu	Trp	Thr	Arg	Gln	Thr	Tyr	Lys	Tyr	Ile	Asp
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Gln	Phe	Phe	Tyr	Ala	Thr	Ala	Ile	Gln	Ala	Gln	Trp	Asn	Lys	Thr	Pro
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Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met	
35 40 45	
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Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu	
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Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val	
65 70 75 80	

aaa aaa cag tat ccg ccg caa acg aaa aaa gcc ggc tat ctg aaa acc 288
 Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr
 85 90 95
 aag gaa gaa ctg ctt gcg gaa ttg gct tgc ctt aaa gcg gaa atg gct 336
 Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala
 100 105 110
 gcc cta aaa aag ctc gat gcc tta atc tat ggg aaa gaa gtg cgg cag 384
 Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln
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 aaa gaa cgc aac tcg tcg cag ggt taa 411
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 130 135

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 Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu
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 Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val
 65 70 75 80
 Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr
 85 90 95
 Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala
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 130 135

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Ser	His	Ala	Asp	Trp	Val	Ile	Thr	Gly	Val	Pro	Tyr	Asp	Met	Ala	Val	
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Lys Lys Asp
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Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val
35 40 45

Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
50 55 60

Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
65 70 75 80

Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
85 90 95

Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly
100 105 110

Lys Leu Leu Ser Ser Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His
115 120 125

Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys
130 135 140

Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly
145 150 155 160

Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly
165 170 175

Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His
180 185 190

Ser Lys Lys Leu Pro Phe Thr Val Leu Thr Ala Pro Gln Val Asn Glu
195 200 205

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
210 215 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
225 230 235 240

Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg
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Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met
 260. , , 265 270

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Lys Lys Asp
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att ccc tac ccc gtc acc agg cgg att gcc tca agt ttg tat tcg acc 96
 Ile Pro Tyr Pro Val Thr Arg Arg Ile Ala Ser Ser Leu Tyr Ser Thr
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gaa tat ttt gtc gta tgc ttt ctg cgt ttg atg cca ctc tct ccg tgt 144
 Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys
 35 40 45

aat ctg tat ttt gtc acc cat ctg cgt acc aat gaa tcg gaa ata gaa 192
 Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu
 50 55 60

aga tgg tct gct gtt ccc tgc caa ata gta ttg aac gac ggc aag tcg 240
 Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser
 65 70 75 80

gaa ttc ggc gga ttc gca ttt gaa gtg caa ctt tcc cta aca gaa aaa 288
 Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys
 85 90 95

ggc cag tat gcg gta gca tac gac ctt tcc tgc aag aaa gat tgc cat 336
 Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His
 100 105 110

gag cta cac gca act gac cca agg cga acg ata cca cat cca ata cct 384
 Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro
 115 120 125

gtc ccg cca ctg cac cgt cac cga aat cgc caa aca gct taa 426
 Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala
 130 135 140

<210> 26
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Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu
50 55 60
Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser
65 70 75 80
Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys
85 90 95
Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His
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Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro
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Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala
130 135 140

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ggg att atg ctg ttg aag gta gta cct gag cgt acc gtt tcg gca gat 96
Gly Ile Met Leu Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp
20 25 30
gca aaa acc aga gac ccg atg tgg gac aat gcg gct tta cag acc agc 144
Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser
35 40 45
gaa ggc gta aat ttt att gct cgt ttc cta gga ttt ttt agc gat ggg 192
Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly
50 55 60
gaa tac cgc tat gtg gat gtc ctg caa ccc aac cat tcc gat att att 240
Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile
65 70 75 80
cgg tat tca ggt aaa gat ttt ccg cta aat caa ata ctt aac cat ata 288
Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile
85 90 95
cac ccc gcc cgt tat gcg gta acg ttc gaa aac aat gtc gat tcc aag 336
His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys

098043-081601

ctg cgc agg cac tga
 Leu Arg Arg His
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351

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 <213> Neisseria meningitidis

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 Gly Ile Met Leu Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp
 20 25 30
 Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser
 35 40 45
 Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly
 50 55 60
 Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile
 65 70 75 80
 Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile
 85 90 95
 His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys
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 Leu Arg Arg His
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 <213> Neisseria meningitidis

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 tgc ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tcg gct atg 96
 Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
 20 25 30
 aaa tcc tat ttt tcc aaa tat atc cta ccc gtt tca ctt ttt acc ttg 144
 Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
 35 40 45
 cca cta tcc ctt tcc cca tcc gtt tcg gct ttt acg ctg cct gaa gca 192
 Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
 50 55 60
 tgg cgg gcg gcg cag caa cat tcg gct gat ttt caa gcg tcc cat tac 240

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Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
65 . . , '70 75 80

cag cgt gat gca gtg cgc gca cgg caa caa caa gcc aag gcc gca ttc 288
Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
85 90 95

ctt ccc cat gta tcc gcc aat gcc agc tac cag cgc cag ccg cca tcg 336
Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
100 105 110

att tct tcc acc cgc gaa aca cag gga tgg agc gtg cag gtg gga caa 384
Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
115 120 125

acc tta ttt gac gct gcc aaa ttt gca caa tac cgc caa agc agg ttc 432
Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
130 135 140

gat acg cag gct gca gaa cag cgt ttc gat gcg gca cgc gaa gaa ttg 480
Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
145 150 155 160

ctg ttg aaa gtt gcc gaa agt tat ttc aac gtt tta ctc agc cga gac 528
Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
165 170 175

acc gtt gcc gcc cat gcg gcg gaa aaa gag gct tat gcc cag cag gta 576
Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
180 185 190

agg cag gcg cag gct tta ttc aat aaa ggt gct gcc acc gcg ctg gat 624
Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
195 200 205

att cac gaa gcc aaa gcc ggt tac gac aat gcc ctg gcc caa gaa atc 672
Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
210 215 220

gcc gta ttg gct gag aaa caa acc tat gaa aac cag ttg aac gac tac 720
Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
225 230 235 240

acc gac ctg gat agc aaa caa atc gag gcc ata gat acc gcc aac ctg 768
Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
245 250 255

ttg gca cgc tat ctg ccc aag ctg gaa cgt tac agt ctg gat gaa tgg 816
Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
260 265 270

cag cgc att gcc tta tcc aac aat cat gaa tac cgg atg cag cag ctt 864
Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
275 280 285

gcc ctg caa agc agc gga cag gcg ctt cgg gca gca cag aac agc cgc 912
Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
290 295 300

tat ccc acc gtt tct gcc cat gtc gcc tat cag aat aac ctc tac act 960
Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
305 310 315 320

tca tct gcg cag aat aat gac tac cac tat cgg gcc aaa ggg atg agc 1008
Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
325 330 335

093043-06101
"0930" E40E360

gtc ggc gta cag•ttg, aat ttg ccg ctt tat acc ggc gga gaa ttg tcg 1056
Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
340 345 350

ggc aaa atc cat gaa gcc gaa gcg caa tac ggg gcc gcc gaa gca cag 1104
Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
355 360 365

ctg acc gca acc gag cgg cac atc aaa ctc gcc gta cgc cag gct tat 1152
Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
370 375 380

acc gaa agc ggt gcg gcg cgt tac caa atc atg gcg caa gaa cgg gtt 1200
Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
385 390 395 400

ttg gaa agc agc cgt ttg aaa ctg aaa tcg acc gaa acc ggc caa caa 1248
Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
405 410 415

tac ggc atc cgc aac cgg ctg gaa gta ata cgg gcg cgg cag gaa gtc 1296
Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
420 425 430

gcc caa gca gaa cag aaa ctg gct caa gca cgg tat aaa ttc atg ctg 1344
Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
435 440 445

gct tat ttg cgc ttg gtg aaa gag agc ggg tta ggg ttg gaa acg gta 1392
Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
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Phe Ala Glu
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<213> Neisseria meningitidis

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Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
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Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
35 40 45
Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
50 55 60
Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
65 70 75 80
Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
85 90 95
Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
100 105 110
Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln

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003043-01601

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130					135						140				
Asp	Thr	Gln	Ala	Ala	Glu	Gln	Arg	Phe	Asp	Ala	Ala	Arg	Glu	Glu	Leu
145					150					155					160
Leu	Leu	Lys	Val	Ala	Glu	Ser	Tyr	Phe	Asn	Val	Leu	Leu	Ser	Arg	Asp
				165					170					175	
Thr	Val	Ala	Ala	His	Ala	Ala	Glu	Lys	Glu	Ala	Tyr	Ala	Gln	Gln	Val
			180					185					190		
Arg	Gln	Ala	Gln	Ala	Leu	Phe	Asn	Lys	Gly	Ala	Ala	Thr	Ala	Leu	Asp
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Ile	His	Glu	Ala	Lys	Ala	Gly	Tyr	Asp	Asn	Ala	Leu	Ala	Gln	Glu	Ile
210					215						220				
Ala	Val	Leu	Ala	Glu	Lys	Gln	Thr	Tyr	Glu	Asn	Gln	Leu	Asn	Asp	Tyr
225					230					235					240
Thr	Asp	Leu	Asp	Ser	Lys	Gln	Ile	Glu	Ala	Ile	Asp	Thr	Ala	Asn	Leu
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Leu	Ala	Arg	Tyr	Leu	Pro	Lys	Leu	Glu	Arg	Tyr	Ser	Leu	Asp	Glu	Trp
			260					265					270		
Gln	Arg	Ile	Ala	Leu	Ser	Asn	Asn	His	Glu	Tyr	Arg	Met	Gln	Gln	Leu
		275					280					285			
Ala	Leu	Gln	Ser	Ser	Gly	Gln	Ala	Leu	Arg	Ala	Ala	Gln	Asn	Ser	Arg
		290				295					300				
Tyr	Pro	Thr	Val	Ser	Ala	His	Val	Gly	Tyr	Gln	Asn	Asn	Leu	Tyr	Thr
305					310					315					320
Ser	Ser	Ala	Gln	Asn	Asn	Asp	Tyr	His	Tyr	Arg	Gly	Lys	Gly	Met	Ser
				325					330					335	
Val	Gly	Val	Gln	Leu	Asn	Leu	Pro	Leu	Tyr	Thr	Gly	Gly	Glu	Leu	Ser
			340					345					350		
Gly	Lys	Ile	His	Glu	Ala	Glu	Ala	Gln	Tyr	Gly	Ala	Ala	Glu	Ala	Gln
		355					360					365			
Leu	Thr	Ala	Thr	Glu	Arg	His	Ile	Lys	Leu	Ala	Val	Arg	Gln	Ala	Tyr
		370				375					380				
Thr	Glu	Ser	Gly	Ala	Ala	Arg	Tyr	Gln	Ile	Met	Ala	Gln	Glu	Arg	Val
385					390					395					400
Leu	Glu	Ser	Ser	Arg	Leu	Lys	Leu	Lys	Ser	Thr	Glu	Thr	Gly	Gln	Gln
				405					410					415	
Tyr	Gly	Ile	Arg	Asn	Arg	Leu	Glu	Val	Ile	Arg	Ala	Arg	Gln	Glu	Val
			420					425					430		
Ala	Gln	Ala	Glu	Gln	Lys	Leu	Ala	Gln	Ala	Arg	Tyr	Lys	Phe	Met	Leu
		435					440					445			
Ala	Tyr	Leu	Arg	Leu	Val	Lys	Glu	Ser	Gly	Leu	Gly	Leu	Glu	Thr	Val
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Phe	Ala	Glu													

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 <212> DNA
 <213> *Neisseria meningitidis*

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aca ttg ggc att tgc gcg ctt tta gcc ttt tgt ttt ggc gcg gcc atc 96
 Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
 20 25 30

gca tca ggt tat cac ttg gaa tat gaa tac ggc tac cgt tat tct gcc 144
 Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala
 35 40 45

gtg ggt gct ttg gct tcg gtt gta ttt tta tta tta ttg gca cgc ggt 192
 Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly
 50 55 60

ttc ccg cgc gtt tct tca gtt gtt tta ctg att tac gtc ggc aca acc 240
 Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr
 65 70 75 80

gcc cta tat ttg ccg gtc ggc tgg ctg tat ggt gcg ccg tct tat cag 288
 Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln
 85 90 95

ata gtc ggt tcg ata ttg gaa agc aat cct gcc gag gcg cgt gaa ttt 336
 Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe
 100 105 110

gtc ggc aat ctt ccc ggg tcg ctt tat ttt gtg cag gca tta ttt ttc 384
 Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe
 115 120 125

att ttt ggc ttg aca gtt tgg aga tat tgt gta tcg ggg ggg gta ttt 432
 Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe
 130 135 140

gct gac gta aaa aac tat aaa cgc cgc agc aaa ata tgg ctg act ata 480
 Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile
 145 150 155 160

tta ttg act ttg att ttg tcc tgc gcg gtg atg gat aaa atc gcc agc 528
 Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser
 165 170 175

gat aaa gat ttg cga gaa cct gat gcc ggc ctg ttg ttg aat att ttc 576
 Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe
 180 185 190

gac ctg tat tac gat ttg gct tcc gcg ccg gca cca ata tgt cgc caa 624
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 195 200 205

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1				5					10					15			
acc	aaa	ggg	ctg	ttg	ata	aac	ggt	tac	cat	ttc	acc	gcc	cac	gcg	acg		96
Thr	Lys	Gly	Leu	Leu	Ile	Asn	Gly	Tyr	His	Phe	Thr	Ala	His	Ala	Thr		
			20					25					30				
aat	ctt	tcg	ctg	ccg	cag	act	ttg	ggg	ctg	ccg	gga	gag	ccg	aac	aat		144
Asn	Leu	Ser	Leu	Pro	Gln	Thr	Leu	Gly	Leu	Pro	Gly	Glu	Pro	Asn	Asn		
		35					40					45					
aac	att	gtc	agc	ttg	gcg	aag	cag	gcg	ggt	ttt	cgg	acg	gcg	tgg	ctg		192
Asn	Ile	Val	Ser	Leu	Ala	Lys	Gln	Ala	Gly	Phe	Arg	Thr	Ala	Trp	Leu		
	50					55					60						
tct	aat	caa	gga	atg	ttg	ggg	cat	ttt	gcc	aac	gaa	att	tcc	acc	tat		240
Ser	Asn	Gln	Gly	Met	Leu	Gly	His	Phe	Ala	Asn	Glu	Ile	Ser	Thr	Tyr		
	65				70				75						80		
gcc	cta	cgc	agc	gat	tat	ccg	tgg	ttt	acc	caa	agg	ggt	gat	tat	ggc		288
Ala	Leu	Arg	Ser	Asp	Tyr	Pro	Trp	Phe	Thr	Gln	Arg	Gly	Asp	Tyr	Gly		
			85						90					95			
aaa	agc	gcg	ggg	ttg	agc	gac	cgc	ctt	ttg	ttg	ccg	gcg	ttc	aaa	cgg		336
Lys	Ser	Ala	Gly	Leu	Ser	Asp	Arg	Leu	Leu	Leu	Pro	Ala	Phe	Lys	Arg		
			100					105					110				
gtt	ttg	ata	gga	aat	gca	ggc	acg	aag	cct	cgg	ctg	att	gtg	atg	cac		384
Val	Leu	Ile	Gly	Asn	Ala	Gly	Thr	Lys	Pro	Arg	Leu	Ile	Val	Met	His		
		115					120					125					
ctg	atg	ggt	tcg	cac	agt	gat	ttt	tgc	aca	cgt	ttg	gat	aag	gat	gcg		432
Leu	Met	Gly	Ser	His	Ser	Asp	Phe	Cys	Thr	Arg	Leu	Asp	Lys	Asp	Ala		
	130					135					140						
cgg	cgg	ttt	cag	tat	caa	act	gaa	aaa	ata	tcc	tgc	tat	gtt	tcc	acc		480
Arg	Arg	Phe	Gln	Tyr	Gln	Thr	Glu	Lys	Ile	Ser	Cys	Tyr	Val	Ser	Thr		
	145				150					155					160		
atc	gcg	caa	acc	gat	aaa	ttt	tta	gaa	gat	aca	gtt	aag	ata	ttg	aat		528
Ile	Ala	Gln	Thr	Asp	Lys	Phe	Leu	Glu	Asp	Thr	Val	Lys	Ile	Leu	Asn		
				165					170					175			
gaa	aat	aaa	gaa	agc	tgg	tct	ttg	gtt	tac	ttt	tcc	gac	cac	ggt	ttg		576
Glu	Asn	Lys	Glu	Ser	Trp	Ser	Leu	Val	Tyr	Phe	Ser	Asp	His	Gly	Leu		
			180					185					190				
atg	cat	gtc															

cgc gga ttc ggc agt tgg acg ggt atc gaa acc gac gag ttg ccc gat 768
 Arg Gly Phe Gly Ser Trp Thr Gly Ile Glu Thr Asp Glu Leu Pro Asp
 245 250 255
 gac ggc tat gat ttt tgg ggg aat gtt ccc gat gtg cag ggc gaa ggc 816
 Asp Gly Tyr Asp Phe Trp Gly Asn Val Pro Asp Val Gln Gly Glu Gly
 260 265 270
 aat aac ctt gcc ttt atc gac gga ctg ccc gac gac ccc gcg ccg tgg 864
 Asn Asn Leu Ala Phe Ile Asp Gly Leu Pro Asp Asp Pro Ala Pro Trp
 275 280 285
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 Tyr Ala Gly Lys Gly Lys Ser Thr Lys Asn Thr Ser Lys Lys
 290 295 300

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 <213> Neisseria meningitidis

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 35 40 45
 Asn Ile Val Ser Leu Ala Lys Gln Ala Gly Phe Arg Thr Ala Trp Leu
 50 55 60
 Ser Asn Gln Gly Met Leu Gly His Phe Ala Asn Glu Ile Ser Thr Tyr
 65 70 75 80
 Ala Leu Arg Ser Asp Tyr Pro Trp Phe Thr Gln Arg Gly Asp Tyr Gly
 85 90 95
 Lys Ser Ala Gly Leu Ser Asp Arg Leu Leu Leu Pro Ala Phe Lys Arg
 100 105 110
 Val Leu Ile Gly Asn Ala Gly Thr Lys Pro Arg Leu Ile Val Met His
 115 120 125
 Leu Met Gly Ser His Ser Asp Phe Cys Thr Arg Leu Asp Lys Asp Ala
 130 135 140
 Arg Arg Phe Gln Tyr Gln Thr Glu Lys Ile Ser Cys Tyr Val Ser Thr
 145 150 155 160
 Ile Ala Gln Thr Asp Lys Phe Leu Glu Asp Thr Val Lys Ile Leu Asn
 165 170 175
 Glu Asn Lys Glu Ser Trp Ser Leu Val Tyr Phe Ser Asp His Gly Leu
 180 185 190
 Met His Val Gly Lys Gly Gly Glu Arg Thr Leu Thr His Gly Ala Trp
 195 200 205
 Lys Arg Gln Ser Tyr Gly Val Pro Leu Val Lys Ile Ser Ser Asp Asp
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 Thr Arg Arg Glu Met Ile Lys Val Arg Arg Ser Ala Phe Asn Phe Leu

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gaa	tcg	aat	ccg	ctt	gcc	gtc	gcc	ggc	tgc	gtc	aat	gct	tat	ttt	gca	96	
Glu	Ser	Asn	Pro	Leu	Ala	Val	Ala	Gly	Cys	Val	Asn	Ala	Tyr	Phe	Ala		
			20					25					30				
cga	ttg	gcc	acc	caa	agc	ggc	ttc	aaa	gcc	atc	tat	ctg	tcc	ggc	ggc	144	
Arg	Leu	Ala	Thr	Gln	Ser	Gly	Phe	Lys	Ala	Ile	Tyr	Leu	Ser	Gly	Gly		
		35					40					45					
ggc	gtg	gca	gcc	tgt	tct	tgc	ggc	atc	cct	gat	ttg	ggc	att	acc	aca	192	
Gly	Val	Ala	Ala	Cys	Ser	Cys	Gly	Ile	Pro	Asp	Leu	Gly	Ile	Thr	Thr		
	50					55					60						
atg	gaa	gat	gtg	ctg	atc	gac	gca	cga	cgc	att	acg	gac	aac	gtg	gat	240	
Met	Glu	Asp	Val	Leu	Ile	Asp	Ala	Arg	Arg	Ile	Thr	Asp	Asn	Val	Asp		
65					70					75					80		
acg	cct	ctg	ctg	gtg	gac	atc	gat	gtg	ggc	tgg	ggc	ggc	gca	ttc	aat	288	
Thr	Pro	Leu	Leu	Val	Asp	Ile	Asp	Val	Gly	Trp	Gly	Gly	Ala	Phe	Asn		
				85					90					95			
att	gcc	cgt	acc	att	cgc	aac	ttt	gaa	cgc	gcc	ggc	ggt	gca	gcg	ggt	336	
Ile	Ala	Arg	Thr	Ile	Arg	Asn	Phe	Glu	Arg	Ala	Gly	Val	Ala	Ala	Val		
			100					105					110				
cac	atc	gaa	gat	cag	gta	gcg	caa	aaa	cgc	tgc	ggc	cac	cgt	ccg	aac	384	
His	Ile	Glu	Asp	Gln	Val	Ala	Gln	Lys	Arg	Cys	Gly	His	Arg	Pro	Asn		
		115					120					125					
aaa	gcc	att	gta	tct	aaa	gat	gaa	atg	gtc	gac	cgt	atc	aaa	gct	gcc	432	
Lys	Ala	Ile	Val	Ser	Lys	Asp	Glu	Met	Val	Asp	Arg	Ile	Lys	Ala	Ala		
	130					135					140						
gta	gat	gcg	cgc	ggt	gat	gag	aac	ttc	gtg	att	atg	gcg	cgt	acc	gat	480	
Val	Asp	Ala	Arg	Val	Asp	Glu	Asn	Phe	Val	Ile	Met	Ala	Arg	Thr	Asp		
145					150					155					160		

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Ala Leu Ala Val-Glu, Gly Leu Asp Ala Ala Ile Glu Arg Ala Gln Ala
165 170 175

tgt gtc gaa gcc ggt gcg gac atg att ttc cct gaa gcc atg acc gat 576
Cys Val Glu Ala Gly Ala Asp Met Ile Phe Pro Glu Ala Met Thr Asp
180 185 190

ttg aac atg tac cgc caa ttt gca gat gcg gtg aaa gtg ccc gtg ttg 624
Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu
195 200 205

gcg aac att acc gag ttt ggt tcc act ccg ctt tat acc caa agc gag 672
Ala Asn Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu
210 215 220

ctg gct gaa aac ggc gtg tcg ctg gtg ctg tat ccg ctg tca tcg ttc 720
Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe
225 230 235 240

cgt gca gca agc aaa gcc gct ctg aat gtt tac gaa gcg att atg cgc 768
Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg
245 250 255

gat ggc act tca ggc ggc ggt ggt gga cag tat gca aac ccg tgc cga 816
Asp Gly Thr Ser Gly Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg
260 265 270

gct gta cga gca tct gaa cta tca tgc ctt cga gca aaa act gga taa 864
Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly
275 280 285

<210> 36
<211> 287
<212> PRT
<213> Neisseria meningitidis

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Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly
35 40 45
Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr
50 55 60
Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp
65 70 75 80
Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn
85 90 95
Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Ala Val
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His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn
115 120 125
Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala
130 135 140

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atg	gac	gtg	atg	cgt	acc	ggc	gta	tcc	atg	ctg	ggc	tgt	gtt	cat	cct	480		
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Gly	His	Phe	Leu	His	Leu	Leu	His	Gly	Lys	Arg	Pro	Ser	Glu	Ser	His			
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Leu Leu Met Gly Ile Phe Leu Ala Val Ser Ala Ala Leu Leu Asn Ala	
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Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val	
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Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser	
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Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser	
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Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Leu Lys Val Ala Ile Cys	
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Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr	
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Gln Tyr Gly Asn Ala Ala Asn Val Val Val Val Leu Met Ala Ser Ala	
115 120 125	
gcc gta tct gcc ttg ata ttg gac agc ata ctg tta gat gaa cgt att	432
Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile	
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tgc att tct tca gtc gtc ggt gtg ggt ttg gca gta ttg ggg atc gca	480
Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala	
145 150 155 160	
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Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala	
165 170 175	
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Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys	
180 185 190	
ttc ggc cta aac ggc ggt att tat ttg aca cgg ata ttg atg ttt ttt	624
Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe	
195 200 205	
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Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile	
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His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu	
225 230 235 240	
ccg acg att tta gga ttt tat tgt aca act aaa gca ttg gat tat ttg	768
Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu	
245 250 255	
agt gct gcg aag gta cag gta act gaa ttg gcc gag cca ttg ttt gct	816
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Thr	Ile	Gly	Ile	Phe	Ser	Lys	Ile	Leu	Met	Glu	Gln	Gly	Leu	Ser	Val	
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Gln	His	Ile	Ala	Phe	Leu	Lys	Thr	Leu	Thr	Gly	Phe	Val	Phe	Ile	Ser	
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Ile	Leu	Leu	Cys	Arg	Thr	Gly	Phe	Thr	Arg	Gln	Ile	Ala	Asp	Ile	Ser	
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Arg	Lys	Lys	Glu	Ala	Ile	Leu	Pro	Leu	Leu	Leu	Lys	Val	Ala	Ile	Cys	
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Ala	Phe	Phe	Gly	Ile	Tyr	Thr	Leu	Phe	Phe	Phe	Glu	Thr	Thr	Ala	Tyr	
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Gln	Tyr	Gly	Asn	Ala	Ala	Asn	Val	Val	Val	Val	Leu	Met	Ala	Ser	Ala	
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Ala	Leu	Ala	Gly	Ser	Gly	Tyr	Gly	Cys	Phe	Ser	Val	Leu	Ile	Lys	Lys	
			180					185					190			
Phe	Gly	Leu	Asn	Gly	Gly	Ile	Tyr	Leu	Thr	Arg	Ile	Leu	Met	Phe	Phe	
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Ile Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val	
180 185 190	
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Lys Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His	
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Thr Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly	
210 215 220	
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Leu Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu	
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Pro Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Gln Ala Gly Ile	
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Thr Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu	
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Arg Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser	
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Gly Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr	
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Leu Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr	
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Ala Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala	
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Ser Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met	
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ccc gac ggc gcg gtc atc atc gcc gcg att acc agt tgc acc aac act	1248
Pro Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr	
405 410 415	
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ccc gaa atg gaa aaa ctc ggc ttc ggt atc gtc gcc ttc gcc tgc acc 1440
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 Ser Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe
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 Pro Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu
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 675 680 685

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Arg Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Lys Asn	
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Ser	Pro 530	Pro	Leu	Val	Val	Ala 535	Tyr	Ala	Leu	Ala	Gly 540	Ser	Ile	Arg	Phe
Asp 545	Ile	Glu	Asn	Asp	Val 550	Leu	Gly	Val	Ala	Asp 555	Gly	Lys	Glu	Ile	Arg 560
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Val	Ser	Ala	Ala 660	Gly	Glu	Tyr	Leu	Ala 665	Lys	Met	Gly	Leu	Pro 670	Glu	Glu
Asp	Phe	Asn	Ser	Tyr	Ala	Thr	His 680	Arg	Gly	Asp	His	Leu 685	Thr	Ala	Gln
Arg 690	Ala	Thr	Phe	Ala	Asn	Pro 695	Lys	Leu	Phe	Asn	Glu 700	Met	Val	Lys	Asn
Glu 705	Asp	Gly	Ser	Val	Arg 710	Gln	Gly	Ser	Phe	Ala 715	Arg	Val	Glu	Pro	Glu 720
Gly	Glu	Thr	Met	Arg 725	Met	Trp	Glu	Ala	Ile 730	Glu	Thr	Tyr	Met	Asn 735	Arg
Lys	Gln	Pro	Leu 740	Ile	Ile	Ile	Ala	Gly 745	Ala	Asp	Tyr	Gly	Gln 750	Gly	Ser
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765

<400>	43																
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Met	Pro	Gln	Ile	Lys	Ile	Pro	Ala	Val	Tyr	Tyr	Arg	Gly	Gly	Thr	Ser		
1				5					10					15			
aaa	ggc	gtg	ttt	ttc	aaa	cgt	tcc	gac	ctg	ccc	gag	gcg	gcg	cgg	gaa		96
Lys	Gly	Val	Phe	Phe	Lys	Arg	Ser	Asp	Leu	Pro	Glu	Ala	Ala	Arg	Glu		
			20					25					30				
gcg	gga	agc	gca	cgc	gac	aaa	atc	ctc	ttg	cgc	gta	ctc	ggc	agc	ccg		144
Ala	Gly	Ser	Ala	Arg	Asp	Lys	Ile	Leu	Leu	Arg	Val	Leu	Gly	Ser	Pro		
		35					40					45					
gac	ccc	tac	ggc	aag	cag	ata	gac	ggg	ttg	ggc	aac	gcc	agt	tcg	tcc		192
Asp	Pro	Tyr	Gly	Lys	Gln	Ile	Asp	Gly	Leu	Gly	Asn	Ala	Ser	Ser	Ser		
	50					55					60						
acc	agc	aaa	gcc	gtg	att	ttg	gac	aag	tcc	gaa	cgc	acc	gat	cac	gat		240
Thr	Ser	Lys	Ala	Val	Ile	Leu	Asp	Lys	Ser	Glu	Arg	Thr	Asp	His	Asp		
65					70				75					80			
gtc	gat	tac	ctt	ttc	ggg	caa	gtt	tcc	atc	gac	aaa	cct	ttt	gtc	gat		288
Val	Asp	Tyr	Leu	Phe	Gly	Gln	Val	Ser	Ile	Asp	Lys	Pro	Phe	Val	Asp		
				85					90					95			
tgg	agt	ggc	aac	tgc	ggc	aac	ctc	acc	gcc	gcc	gtg	ggc	gca	ttt	gcc		336
Trp	Ser	Gly	Asn	Cys	Gly	Asn	Leu	Thr	Ala	Ala	Val	Gly	Ala	Phe	Ala		
			100					105					110				
atc	gag	caa	ggc	ttg	gtc	gat	aaa	tcc	aaa	atc	cct	tca	gac	ggc	ccg		384
Ile	Glu	Gln	Gly	Leu	Val	Asp	Lys	Ser	Lys	Ile	Pro	Ser	Asp	Gly	Pro		
		115					120					125					

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tgt acc gtc aaa .atc, tgg cag aaa aac atc ggc aaa acc att att gcc	432
Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala	
130 135 140	
cat gta ccg atg caa aac ggc gca gtt ttg gaa aca ggc gat ttt gag	480
His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu	
145 150 155 160	
ctc gac ggc gta acg ttc ccg gca gcc gaa gta' caa atc gaa ttt ctt	528
Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu	
165 170 175	
gat cca gcc gac ggc gaa ggc agt atg ttc cca acc ggc aat ttg gtc	576
Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val	
180 185 190	
gat gaa att gat gtg ccg aat ata ggc cgt ttg aaa gcc acg ctc atc	624
Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile	
195 200 205	
aac gcg ggc att ccg acc gtt ttc ctg aat gcc gcc gac ttg ggc tac	672
Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr	
210 215 220	
acg ggc aaa gag ttg caa gac gac atc aac aac gat gcc gca gct ttg	720
Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu	
225 230 235 240	
gaa aaa ttc gag aaa atc cgc gct tac ggt gcg ctg aaa atg ggt cta	768
Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu	
245 250 255	
atc agc gac gta tcc gaa gct gcc gcc cgc gcg cac acg ccg aaa gtc	816
Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val	
260 265 270	
gcc ttc gtc gcg ccc gcc gcc gat tac acc gcc tcc agt ggc aaa acc	864
Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr	
275 280 285	
gtg aat gcc gcc gac atc gat ttg ctg gta cgc gcc ctg agc atg ggc	912
Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly	
290 295 300	
aaa ttg cac cac gcg atg atg ggt acc gcc tct gtt gcc att gcg acc	960
Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr	
305 310 315 320	
gcc gcc gcc gtg ccc ggt acg ctg gtc aac ctt gcc gca ggg gcg gga	1008
Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Ala Gly	
325 330 335	
acg cgt aaa gaa gtg cgc ttc ggg cat cct tcc ggc aca ttg cgc gtc	1056
Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val	
340 345 350	
ggt gca gcc gcc gaa tgt cag gac gga caa tgg acg gcc acc aaa gcg	1104
Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala	
355 360 365	
gtt atg agc cgc agc gca cgc gtg atg atg gaa ggt tgg gtc agg gtg	1152
Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val	
370 375 380	
ccg gaa gat tgt ttt taa	1170

05830433-061604

Pro Glu Asp Cys Phe
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<210> 44
<211> 389
<212> PRT
<213> Neisseria meningitidis

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Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu
20 25 30
Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
35 40 45
Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
50 55 60
Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp
65 70 75 80
Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
85 90 95
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
100 105 110
Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro
115 120 125
Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala
130 135 140
His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu
145 150 155 160
Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu
165 170 175
Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val
180 185 190
Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile
195 200 205
Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr
210 215 220
Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu
225 230 235 240
Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu
245 250 255
Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val
260 265 270
Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr
275 280 285
Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly
290 295 300

009180-EE40E360

Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr
 305 310 315 320
 Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Ala Gly
 325 330 335
 Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
 340 345 350
 Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala
 355 360 365
 Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val
 370 375 380
 Pro Glu Asp Cys Phe
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<210> 45
 <211> 954
 <212> DNA
 <213> Neisseria meningitidis

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 Ala Met Leu Pro Ala Cys Trp Ala Gln Ala Met Leu Ala Glu Val Ile
 20 25 30
 agc tgc aac aag gct tcg tcg ctg ccg cag cct tcg gcg aga tcg gcg 144
 Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala
 35 40 45
 ttt aaa tca acc tgc ttc atg ggt gat tct ccg tat ttg gtt cag ata 192
 Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile
 50 55 60
 gac ttg gtt ttt gcg ccg cag ggc ggt ggc ttc ttt caa gcc gat tat 240
 Asp Leu Val Phe Ala Pro Gln Gly Gly Gly Phe Phe Gln Ala Asp Tyr
 65 70 75 80
 ttt gaa ttt gac ttt gct gcc gaa gcg cac ctg tgc cag cct gcc caa 288
 Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln
 85 90 95
 atc ggc ggc ggc aac ggt agc gat ttt cgg ata acc gcc ggt ggt ttg 336
 Ile Gly Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu
 100 105 110
 cgc atc ggc cag cag gat aat cgg ttt gcc gcc ggg cgg cac ctg cac 384
 Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His
 115 120 125
 ggt tcc tgc ctg aac agc gtg gga cag cat ttc caa agg ttg cga cag 432
 Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln
 130 135 140

009430 E4000000

Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln
 85 90 95
 Ile Gly Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu
 100 105 110
 Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His
 115 120 125
 Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln
 130 135 140
 Gly Gln Arg Leu Ser Val Glu Ala Val Ala His Ala Val Ala Ile Ala
 145 150 155 160
 Leu Gln Arg Pro Arg Phe Pro Phe Gln Ile Gln Thr Pro Phe Phe Thr
 165 170 175
 Glu Ser Gly Ile Phe Arg Arg Arg Asn Lys Val Asp Gly Ile Gly Lys
 180 185 190
 Arg Tyr Arg Gly Asn Ala Asp Phe Gly Gln Phe Leu Arg Thr Phe Ala
 195 200 205
 Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala
 210 215 220
 Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His
 225 230 235 240
 Ile Lys Ser Ala Arg His Ala His Ile Ala Val His Ala Leu His Gly
 245 250 255
 Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile
 260 265 270
 Arg Ile Asp Arg Phe Ala Val Gln Phe Arg Leu Ile His Gly Thr Gly
 275 280 285
 Glu Thr Lys Arg Arg Ile Pro Phe Lys His Gln His Tyr Pro Ala Gln
 290 295 300
 Ser Asp Phe Asp Cys Gly Arg Ala Phe Val Val Ala Gln
 305 310 315

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 <211> 648
 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> CDS
 <222> (1)..(645)

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 ctg aat gcg cct tcc gaa ctg ggc aaa cag caa aag ttg tgg gcg ttt 96
 Leu Asn Ala Pro Ser Glu Leu Gly Lys Gln Gln Lys Leu Trp Ala Phe
 20 25 30

038330433-031604

gcc Ala	gct Ala	gcg Ala	ctc Leu	ggg Gly	cag Gln	cac His	gac Asp	agg Arg	att Ile	gag Glu	gaa Glu	gtg Val	gtg Val	gtc Val	ggc Gly	144
354045																
atg Met	aac Asn	aat Asn	ctg Leu	acc Thr	gtg Val	ttc Phe	acc Thr	cgt Arg	ttc Phe	gat Asp	acc Thr	gat Asp	ttg Leu	gcg Ala	acg Thr	192
505560																
ctt Leu	gcc Ala	gat Asp	gaa Glu	ttg Leu	caa Gln	tat Tyr	gtg Val	tgg Trp	gaa Glu	cac His	acc Thr	gcc Ala	gtt Val	aca Thr	gac Asp	240
65707580																
cat His	cag Gln	ggc Gly	aaa Lys	ctg Leu	gtg Val	gaa Glu	att Ile	ccc Pro	gtc Val	tgc Cys	tac Tyr	ggc Gly	ggc Gly	gaa Glu	tac Tyr	288
859095																
ggc Gly	ccg Pro	gat Asp	ttg Leu	gcg Ala	gaa Glu	gtc Val	gct Ala	gct Ala	ttc Phe	cat His	cag Gln	acg Thr	gtt Val	att Ile	tcc Ser	336
100105110																
gaa Glu	atc Ile	gtc Val	cgc Arg	cgc Arg	cat His	acg Thr	gcg Ala	caa Gln	act Thr	tat Tyr	acc Thr	gta Val	ttt Phe	atg Met	atg Met	384
115120125																
ggc Gly	ttc Phe	cag Gln	cct Pro	ggt Gly	ttc Phe	cct Pro	tat Tyr	ctg Leu	ggc Gly	ggc Gly	ttg Leu	ccc Pro	gaa Glu	gca Ala	ttg Leu	432
130135140																
cac His	acg Thr	ccc Pro	cgc Arg	cgt Arg	gcc Ala	gtg Val	ccg Pro	aga Arg	acg Thr	tcc Ser	gtt Val	cct Pro	gcc Ala	ggt Gly	tcg Ser	480
145150155																
gtc Val	ggt Gly	atc Ile	ggc Gly	ggc Gly	agt Ser	cag Gln	acc Thr	ggt Gly	gtg Val	tat Tyr	ccg Pro	ttc Phe	gct Ala	tcg Ser	ccc Pro	528
165170175																
ggc Gly	ggc Gly	tgg Trp	cag Gln	att Ile	atc Ile	ggc Gly	aga Arg	acc Thr	gaa Glu	tta Leu	ccc Pro	ttg Leu	ttc Phe	cga Arg	gcc Ala	576
180185190																
gat Asp	ttg Leu	aat Asn	ccg Pro	ccg Pro	acc Thr	ctg Leu	ctg Leu	gcg Ala	gcg Ala	ggt Gly	gac Asp	caa Gln	gtc Val	cgc Arg	ttt Phe	624
195200205																
gtt Val	gca Ala	gaa Glu	agg Arg	att Ile	gag Glu	cca Pro	tga									648
210215																

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<210> 48
<211> 215
<212> PRT
<213> Neisseria meningitidis
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 85 90 95
 Gly Pro Asp Leu Ala Glu Val Ala Ala Phe His Gln Thr Val Ile Ser
 100 105 110
 Glu Ile Val Arg Arg His Thr Ala Gln Thr Tyr Thr Val Phe Met Met
 115 120 125
 Gly Phe Gln Pro Gly Phe Pro Tyr Leu Gly Gly Leu Pro Glu Ala Leu
 130 135 140
 His Thr Pro Arg Arg Ala Val Pro Arg Thr Ser Val Pro Ala Gly Ser
 145 150 155 160
 Val Gly Ile Gly Gly Ser Gln Thr Gly Val Tyr Pro Phe Ala Ser Pro
 165 170 175
 Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala
 180 185 190
 Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe
 195 200 205
 Val Ala Glu Arg Ile Glu Pro
 210 215

<210> 49
 <211> 930
 <212> DNA
 <213> Neisseria meningitidis

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 <222> (1)..(927)

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 Met Ile His Val Ser Ala Val Gln Ala Pro Ala His Ile Gln Asp Thr
 1 5 10 15
 gga cgc tac gga cac cgg cgt tac ggc atc ggt cat gcc ggt gcg atg 96
 Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met
 20 25 30
 gac acg gtt gct ttg gcg gcg ggt aat att tta ttg ggc aac gac gaa 144
 Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Gly Asn Asp Glu
 35 40 45
 ggc acg gcc gca atc gaa atc gct ttg ggc ggg ata atg ctg gtg ttt 192
 Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe
 50 55 60
 gaa cgg gat acg ccg ttt tgt ctc acc ggt gcc gtg tat cag gcg gaa 240
 Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu
 65 70 75 80
 ttg gac ggc gaa ccg gtc tat tcg tat tgg cgt tat acc gcc cgc aaa 288
 Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys
 85 90 95

09030433.081601

[illegible]

<210> 50

<212> PRT

<400> 50

1

5

10

15

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 35 40 45
 Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe
 50 55 60
 Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu
 65 70 75 80
 Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys
 85 90 95
 Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr
 100 105 110
 Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg
 115 120 125
 Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu
 130 135 140
 Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser
 145 150 155 160
 Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val
 165 170 175
 Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu
 180 185 190
 Glu Arg Glu Thr Trp Thr Leu Gln Ser Asp Ser Asn Arg Met Gly Tyr
 195 200 205
 Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu
 210 215 220
 Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys
 225 230 235 240
 Pro Ile Ile Leu Leu Ala Asp Ala Gln Thr Thr Gly Gly Tyr Pro Lys
 245 250 255
 Ile Ala Thr Val Ala Ala Ala Asp Leu Gly Arg Leu Ala Gln Val Arg
 260 265 270
 Phe Gly Ser Lys Val Lys Phe Lys Ile Ile Gly Leu Lys Glu Ala Thr
 275 280 285
 Ala Leu Arg Arg Lys Asn Gln Val Tyr Leu Asn Gln Ile Arg Arg Ile
 290 295 300
 Thr His Glu Ala Gly
 305

<210> 51

<211> 2094

<212> DNA

<213> Neisseria meningitidis

<220>

093043-01601

<221> CDS
 <222> (1)..(2091) , .

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 Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe
 1 5 10 15

ttc gcc tct gga ttc tgc gcc ctg att tac cag gtc agc tgg cag agg 96
 Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
 20 25 30

ctt cta ttc agt cac ata ggt atc gat ttg agt tgc att act gtc att 144
 Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile
 35 40 45

att tct gta ttt atg gtc ggc ttg ggt gta ggt gcg tat ttc ggt gga 192
 Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly
 50 55 60

cgc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc 240
 Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile
 65 70 75 80

gct gaa gta tcc atc ggt ctg ttc ggt ttg gta agc agg ggt ctg att 288
 Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Arg Gly Leu Ile
 85 90 95

tcc ggc ttg ggg cat ctt tta gtt gag gct gat ttg ccc atc atc gct 336
 Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala
 100 105 110

gct gcc aat ttc ctc tta ttg ctg ctt cct acc ttt atg atg ggc gcg 384
 Ala Ala Asn Phe Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala
 115 120 125

acc ttg ccc ttg ctg acc tgt ttt ttt aac cgg aaa ata cat aat gtt 432
 Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val
 130 135 140

ggc gag tct atc ggt acc tta tat ttt ttc aac act ttg ggt gcg gca 480
 Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala
 145 150 155 160

ctc gga tgc ctt gcc gcc gcc gaa ttt ttc tac gtc ttt ttt acc ctc 528
 Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu
 165 170 175

tcc caa acc att gcg ctg aca gcc tgc ttt aac ctt ctg att gct gct 576
 Ser Gln Thr Ile Ala Leu Thr Ala Cys Phe Asn Leu Leu Ile Ala Ala
 180 185 190

tca gta tgc tgc gtt aca gaa agg atg gat ata gtg aac act aaa ccg 624
 Ser Val Cys Cys Val Thr Glu Arg Met Asp Ile Val Asn Thr Lys Pro
 195 200 205

aat act agt ttg att tat atg ctt tct ttc ctt agc ggc tta ttg agc 672
 Asn Thr Ser Leu Ile Tyr Met Leu Ser Phe Leu Ser Gly Leu Leu Ser
 210 215 220

ttg ggt ata gaa gtc ttg tgg gta agg atg ttt tgc ttc gca gca cag 720
 Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln
 225 230 235 240

tcc gtg cct cag gca ttt tca ttt act ctt gcc tat ttt ctg acc ggt 768
 Ser Val Pro Gln Ala Phe Ser Phe Thr Leu Ala Tyr Phe Leu Thr Gly

093043-08501

245	250	255	
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gtt gat att ccc ttt atc ggg cag tgc ttc ttg tgg gcg ggt att gcc Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala 275 280 285			864
gac ttt ttg att ttg ggt gct gcg tgg ttg ttg acg ggt ttt tcc ggc Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly 290 295 300			912
ttc gtc cac cac gcc ggt atc ttc att acc ctg tct gcc gtc gtc aga Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg 305 310 315 320			960
ggg ttg att ttc ccg ctc gta cac cat gtg ggt acg gat ggc aac aaa Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys 325 330 335			1008
tcc gga cga cag gtt tcc aat gtt tat ttc gcc aac gtt gcc ggc agt Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser 340 345 350			1056
gca ttg ggt ccg gtc ctt atc ggc ttt gtg ata ctt gat ttc ttg tcc Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Phe Leu Ser 355 360 365			1104
acc caa cag att tac ctg ctc atc tgt ttg att tct gct gct gtc cct Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro 370 375 380			1152
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gta gca gtt tcc cta atg ttc ggc atc ctc atg ttc cta ctg ccg gat Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp 405 410 415			1248
tct gtc ttt caa aat att gct gac cgt ccg gat ccg ctg att gaa aac Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn 420 425 430			1296
aaa cac ggc att gtt gcg gtt tac cat aga gat ggt gat aag gtt gtt Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val 435 440 445			1344
tat ggg gcg aat gta tac gac ggc gca tac aat acc gat gta ttc aat Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn 450 455 460			1392
agt gtc aac ggc atc gaa cgt gcc tat ctg cta ccc tcc ctg aag tct Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser 465 470 475 480			1440
ggc ata cgc cgc att ttc gtc gtt gga ttg agt aca ggt tcg tgg gcg Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala 485 490 495			1488
cgc gtc ttg tct gcc att ccg gaa atg cag tcg atg atc gtt gcg gaa Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu 500 505 510			1536

Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile
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 Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Arg Gly Leu Ile
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 Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala
 100 105 110
 Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala
 115 120 125
 Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val
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 Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala
 145 150 155 160
 Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu
 165 170 175
 Ser Gln Thr Ile Ala Leu Thr Ala Cys Phe Asn Leu Leu Ile Ala Ala
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 Ser Val Cys Cys Val Thr Glu Arg Met Asp Ile Val Asn Thr Lys Pro
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 Asn Thr Ser Leu Ile Tyr Met Leu Ser Phe Leu Ser Gly Leu Leu Ser
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 Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln
 225 230 235 240
 Ser Val Pro Gln Ala Phe Ser Phe Thr Leu Ala Tyr Phe Leu Thr Gly
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 Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala
 275 280 285
 Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly
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 Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg
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 Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys
 325 330 335
 Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser
 340 345 350
 Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Phe Leu Ser
 355 360 365
 Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro
 370 375 380
 Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser
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 Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp
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090303-031004

Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn
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 Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val
 435 440 445
 Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn
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 Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser
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 Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala
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 Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu
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 Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala
 515 520 525
 Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg
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 Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met
 545 550 555 560
 Asn Thr Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala
 565 570 575
 Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val
 580 585 590
 Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His
 595 600 605
 Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala
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 Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser
 625 630 635 640
 Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr
 645 650 655
 Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Gln Met
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 690 695

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 <213> Neisseria meningitidis

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Met	Leu 50	Cys	Ala	Gly	Arg	Asp 55	Asp	Val	Ala	Val	Thr 60	Asp	Arg	Asp	Ala
Lys 65	Ile	Asn	Ala	Pro	Pro 70	Pro	Asn	Leu	His	Thr 75	Gly	Asp	Phe	Thr	Asn 80
Pro	Asn	Asp	Ala	Tyr 85	Lys	Asn	Leu	Ile	Asn 90	Leu	Lys	Pro	Ala	Ile 95	Glu
Ala	Gly	Tyr	Thr 100	Gly	Arg	Gly	Val	Glu 105	Val	Gly	Ile	Val	Asp 110	Thr	Gly
Glu	Ser	Val 115	Gly	Ser	Ile	Ser	Phe 120	Pro	Glu	Leu	Tyr	Gly 125	Arg	Lys	Glu
His	Gly 130	Tyr	Asn	Glu	Asn	Tyr 135	Lys	Asn	Tyr	Thr	Ala 140	Tyr	Met	Arg	Lys
Glu 145	Ala	Pro	Glu	Asp	Gly 150	Gly	Gly	Lys	Asp	Ile 155	Lys	Ala	Ser	Phe	Asp 160
Asp	Glu	Ala	Val	Ile 165	Glu	Thr	Glu	Ala	Lys 170	Pro	Thr	Asp	Ile	Arg	His
Val	Lys	Glu	Ile 180	Gly	His	Ile	Asp 185	Val	Val	Ser	His	Ile	Ile 190	Gly	Gly
Arg	Ser	Val 195	Asp	Gly	Arg	Pro	Ala 200	Gly	Gly	Ile	Ala	Pro 205	Asp	Ala	Thr
Leu	His 210	Ile	Met	Asn	Thr	His 215	Asp	Gly	Thr	Lys	Asn 220	Glu	Ile	Met	Ser
Ala 225	Ala	Ile	Arg	Asn	Ala 230	Trp	Val	Lys	Leu	Gly 235	Glu	Arg	Gly	Val	Arg 240
Ile	Val	Asn	Asn	Ser 245	Phe	Gly	Thr	Thr	Ser 250	Arg	Ala	Gly	Thr	Ala 255	Asp
His	Phe	Gln	Ile 260	Ala	Asn	Ser	Glu	Glu 265	Gln	Tyr	Arg	Gln	Ala 270	Leu	Leu
Ala	Tyr	Ser 275	Gly	Gly	Asp	Lys	Thr 280	Asp	Glu	Gly	Ile	Arg 285	Leu	Met	Gln
Gln	Ser 290	Asp	Tyr	Gly	Asn	Leu 295	Ser	Tyr	His	Ile	Arg 300	Asn	Lys	Asn	Met
Leu 305	Phe	Ile	Phe	Ser	Ala 310	Ser	Asn	Asp	Ala	Gln 315	Ala	Gln	Pro	Asn	Thr 320
Leu	Thr	Leu	Leu	Pro 325	Phe	Tyr	Glu	Lys	Asp 330	Ala	Gln	Lys	Gly	Ile 335	Ile
Thr	Val	Ala	Gly 340	Val	Asp	Arg	Ser	Gly 345	Glu	Lys	Phe	Asn	Gly 350	Ser	Asn
His	Cys	Gly 355	Ile	Thr	Ala	Met	Trp 360	Cys	Leu	Ser	Ala	Pro 365	Tyr	Glu	Ala

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Ser 370	Val	Arg	Phe	Thr	Arg	Thr	Asn	Pro	Ile	Gln	Ile	Ala	Gly	Thr	Ser
Phe 385	Ser	Ala	Pro	Ile	Val	Thr	Gly	Thr	Ala	Ala	Leu	Leu	Leu	Gln	Lys 400
Tyr	Pro	Trp	Met	Ser 405	Asn	Asp	Asn	Leu	Arg 410	Thr	Thr	Leu	Leu	Thr 415	Thr
Ala	Gln	Asp	Ile 420	Gly	Ala	Val	Gly	Val 425	Asp	Ser	Lys	Phe	Gly 430	Trp	Gly
Leu	Leu	Asp 435	Ala	Gly	Lys	Ala	Met 440	Asn	Gly	Pro	Ala	Ser 445	Phe	Pro	Phe
Gly	Asp 450	Phe	Thr	Ala	Asp	Thr 455	Lys	Gly	Thr	Ser	Asp 460	Ile	Ala	Tyr	Ser
Phe 465	Arg	Asn	Asp	Ile	Ser 470	Gly	Thr	Gly	Gly	Leu 475	Ile	Lys	Lys	Gly	Gly 480
Ser	Gln	Leu	Gln	Leu 485	His	Gly	Asn	Asn	Thr 490	Tyr	Thr	Gly	Lys	Thr 495	Ile
Ile	Glu	Gly	Gly 500	Ser	Leu	Val	Leu	Tyr 505	Gly	Asn	Asn	Lys	Ser 510	Asp	Met
Arg	Val	Glu 515	Thr	Lys	Gly	Ala	Leu 520	Ile	Tyr	Asn	Gly	Ala 525	Ala	Ser	Gly
Gly	Ser 530	Leu	Asn	Ser	Asp	Gly 535	Ile	Val	Tyr	Leu	Ala 540	Asp	Thr	Asp	Arg
Ser 545	Gly	Ala	Asn	Glu	Thr 550	Val	His	Ile	Lys	Gly 555	Asp	Leu	Gln	Leu	Gly 560
Gly	Glu	Gly	Thr	Leu 565	Tyr	Thr	Arg	Leu	Gly 570	Lys	Leu	Leu	Lys	Val 575	Asp
Gly	Thr	Ala	Met 580	Thr	Gly	Gly	Lys	Leu 585	Tyr	Met	Ser	Ala	Arg 590	Gly	Lys
Gly	Ala	Gly 595	Tyr	Leu	Asn	Arg	Thr 600	Gly	Gln	Arg	Val	Pro 605	Phe	Leu	Ser
Ala	Ala	Lys	Ile	Gly	Arg	Asp 615	Tyr	Ser	Phe	Phe	Thr 620	Asn	Ile	Glu	Thr
Asp 625	Gly	Gly	Leu	Leu	Ala 630	Ser	Leu	Asp	Ser	Val 635	Glu	Lys	Thr	Ala	Gly 640
Ser	Glu	Gly	Asp	Thr 645	Leu	Ser	Tyr	Tyr	Val 650	Arg	Arg	Gly	Asn	Ala 655	Ala
Arg	Thr	Ala	Ser 660	Ala	Ala	Ala	His	Ser 665	Ala	Pro	Ala	Gly	Leu 670	Lys	His
Ala	Val	Glu 675	Gln	Gly	Gly	Ser	Asn 680	Leu	Glu	Asn	Leu	Met 685	Val	Glu	Leu
Asp	Ala 690	Ser	Glu	Ser	Ser	Ala 695	Thr	Pro	Glu	Thr	Val 700	Glu	Thr	Ala	Ala
Ala 705	Asp	Arg	Thr	Asp	Met 710	Pro	Gly	Ile	Arg	Pro 715	Tyr	Gly	Ala	Thr	Phe 720

[illegible]

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His	Ala	Asp	Met	Gln	Gly	Arg	Arg	Leu	Lys	Ala	Val	Ser	Asp	Gly	Leu
		755					760					765			
Asp	His	Asn	Ala	Thr	Gly	Leu	Arg	Val	Ile	Ala	Gln	Thr	Gln	Gln	Asp
	770					775					780				
Gly	Gly	Thr	Trp	Glu	Gln	Gly	Gly	Val	Glu	Gly	Lys	Met	Arg	Gly	Ser
785					790					795					800
Thr	Gln	Thr	Val	Gly	Ile	Ala	Ala	Lys	Thr	Gly	Glu	Asn	Thr	Thr	Ala
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Ala	Ala	Thr	Leu	Gly	Met	Gly	His	Ser	Thr	Trp	Ser	Glu	Asn	Ser	Ala
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Asn	Ala	Lys	Thr	Asp	Ser	Ile	Ser	Leu	Phe	Ala	Gly	Ile	Arg	His	Asp
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Ala	Gly	Asp	Ile	Gly	Tyr	Leu	Lys	Gly	Leu	Phe	Ser	Tyr	Gly	Arg	Tyr
	850					855					860				
Lys	Asn	Ser	Ile	Ser	Arg	Ser	Thr	Gly	Ala	Asp	Glu	His	Ala	Glu	Gly
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Ser	Val	Asn	Gly	Thr	Leu	Met	Gln	Leu	Gly	Ala	Leu	Gly	Gly	Val	Asn
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Val	Pro	Phe	Ala	Ala	Thr	Gly	Asp	Leu	Thr	Val	Glu	Gly	Gly	Leu	Arg
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Tyr	Asp	Leu	Leu	Lys	Gln	Asp	Ala	Phe	Ala	Glu	Lys	Gly	Ser	Ala	Leu
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Gly	Trp	Ser	Gly	Asn	Ser	Leu	Thr	Glu	Gly	Thr	Leu	Val	Gly	Leu	Ala
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Gly	Leu	Lys	Leu	Ser	Gln	Pro	Leu	Ser	Asp	Lys	Ala	Val	Leu	Phe	Ala
945					950					955					960
Thr	Ala	Gly	Val	Glu	Arg	Asp	Leu	Asn	Gly	Arg	Asp	Tyr	Thr	Val	Thr
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Asn	Met	Pro	His	Thr	Arg	Leu	Val	Ala	Gly	Leu	Gly	Ala	Asp	Val	Glu
		995					1000					1005			
Phe	Gly	Asn	Gly	Trp	Asn	Gly	Leu	Ala	Arg	Tyr	Ser	Tyr	Ala	Gly	Ser
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Lys	Gln	Tyr	Gly	Asn	His	Ser	Gly	Arg	Val	Gly	Val	Gly	Tyr	Arg	Phe
1025				1030						1035					1040

Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr
225 230 235 240

agc gga tta ata caa ggt aag ttc att aca acg gaa aaa cct tta aag 768
Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys
245 250 255

aat aat atg aaa ggt att acc ttg ttt gcc aac ggc aga atg gta aat 816
Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn
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<213> Neisseria gonorrhoeae

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His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu
20 25 30

Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg
35 40 45

Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile
50 55 60

Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg
65 70 75 80

Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr
85 90 95

Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys
100 105 110

Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu
115 120 125

Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe
130 135 140

Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr
145 150 155 160

Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val
165 170 175

Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile
180 185 190

Lys Val Ser Leu Asn Gly Ser Glu Pro Arg Ile Ile Asp Gly Asn Leu
195 200 205

Lys Tyr Asn Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu
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Ala	Ser	Glu	Ile	Ala	Tyr	Arg	Phe	Val	Phe	Gly	Ile	Glu	Thr	Leu	Pro		
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Ala	Ala	Lys	Met	Ala	Glu	Thr	Phe	Ala	Leu	Thr	Phe	Met	Ile	Ala	Ala		
		35					40					45					
ctg	tat	ctg	ttt	gcg	cgt	tat	aag	gct	tcg	cgg	ctg	ctg	att	gcg	gtg		192
Leu	Tyr	Leu	Phe	Ala	Arg	Tyr	Lys	Ala	Ser	Arg	Leu	Leu	Ile	Ala	Val		
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ttt	ttc	gcg	ttc	agc	atg	att	gcc	aac	aat	gtg	cat	tac	gcg	gtt	tat		240
Phe	Phe	Ala	Phe	Ser	Met	Ile	Ala	Asn	Asn	Val	His	Tyr	Ala	Val	Tyr		
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caa	agc	tgg	atg	acg	ggg	att	aac	tat	tgg	ctg	atg	ctg	aaa	gag	gtt		288
Gln	Ser	Trp	Met	Thr	Gly	Ile	Asn	Tyr	Trp	Leu	Met	Leu	Lys	Glu	Val		
				85					90					95			
acc	gaa	gtc	ggc	agc	gcg	ggc	gcg	tcg	atg	ttg	gat	aag	ttg	tgg	ctg		336
Thr	Glu	Val	Gly	Ser	Ala	Gly	Ala	Ser	Met	Leu	Asp	Lys	Leu	Trp	Leu		
			100					105					110				
cct	gct	ttg	tgg	ggc	gtg	ggc	gaa	gtc	atg	ttg	ttt	tgc	agc	ctt	gcc		384
Pro	Ala	Leu	Trp	Gly	Val	Ala	Glu	Val	Met	Leu	Phe	Cys	Ser	Leu	Ala		
		115					120					125					
aag	ttc	cgc	cgt	aag	acg	cat	ttt	tct	gcc	gat	ata	ctg	ttt	gcc	ttc		432
Lys	Phe	Arg	Arg	Lys	Thr	His	Phe	Ser	Ala	Asp	Ile	Leu	Phe	Ala	Phe		
	130					135					140						
cta	atg	ctg	atg	att	ttc	gtg	cgt	tcg	ttc	gac	acg	aaa	caa	gag	cac		480
Leu	Met	Leu	Met	Ile	Phe	Val	Arg	Ser	Phe	Asp	Thr	Lys	Gln	Glu	His		
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ggg	att	tcg	ccc	aaa	ccg	aca	tac	agc	cgc	atc	aaa	gcc	aat	tat	ttc		528
Gly	Ile	Ser	Pro	Lys	Pro	Thr	Tyr	Ser	Arg	Ile	Lys	Ala	Asn	Tyr	Phe		
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agc ttc ggt tat ttt gtc ggg cgc gtg ttg ccg tat cag ttg ttt gat	576
Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp	
180 185 190	
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Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly	
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Gln Gly Ser Ile Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser	
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gcg gcg cat ttg aaa ttg ttt ggt tac ggg cgc gaa act tcg ccg ttt	720
Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe	
225 230 235 240	
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Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser	
245 250 255	
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Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn	
260 265 270	
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Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr	
275 280 285	
aat atg ttc cgc ctc gcc aaa gag cag ggc tat gaa acg tat ttt tac	912
Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr	
290 295 300	
agt gcc cag gct gaa aac caa atg gca att ttg aac tta atc ggt aag	960
Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys	
305 310 315 320	
aaa tgg ata gac cat ctg att cag ccg acg caa ctt ggc tac ggc aac	1008
Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn	
325 330 335	
ggc gac aat atg ccc gat gag aag ctg ctg ccg ttg ttc gac aaa atc	1056
Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile	
340 345 350	
aat ttg cag cag ggc agg cat ttt atc gtg ttg cac caa cgc ggt tcg	1104
Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser	
355 360 365	
cac gcc cca tac ggc gca ttg ttg cag cct caa gat aaa gta ttc ggc	1152
His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly	
370 375 380	
gaa gcc gat att gtg gat aag tac gac aac acc atc cac aaa acc gac	1200
Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp	
385 390 395 400	
caa atg att caa acc gta ttc gag cag ctg caa aag cag cct gac ggc	1248
Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly	
405 410 415	
aac tgg ctg ttt gcc tat acc tcc gat cat ggc cag tat gtg cgc caa	1296
Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln	
420 425 430	
gat atc tac aat caa ggc acg gtg cag ccc gac agc tat att gtg cct	1344
Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro	

435

440

445

ctg gtt ttg tac agc ccg gat aag gcc gtg caa cag gct gcc aac cag 1392
 Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln
 450 455 460

gct ttt gcg cct tgc gag att gcc ttc cat cag cag ctt tca acg ttc 1440
 Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe
 465 470 475 480

ctg att cac acg ttg ggc tac gat atg ccg gtt tca ggt tgt cgc gaa 1488
 Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu
 485 490 495

ggc tgc gta aca ggc aac ctg att acg ggc gat gca ggc agc ttg aac 1536
 Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn
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<212> PRT

<213> Neisseria gonorrhoeae

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Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala
 35 40 45

Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val
 50 55 60

Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr
 65 70 75 80

Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val
 85 90 95

Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu
 100 105 110

Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala
 115 120 125

Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe
 130 135 140

Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His
 145 150 155 160

Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe
 165 170 175

Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp
 180 185 190

Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly

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Ala	Ala	His	Leu	Lys	Leu	Phe	Gly	Tyr	Gly	Arg	Glu	Thr	Ser	Pro	Phe
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Leu	Thr	Arg	Leu	Ser	Gln	Ala	Asp	Phe	Lys	Pro	Ile	Val	Lys	Gln	Ser
			245						250					255	
Tyr	Ser	Ala	Gly	Phe	Met	Thr	Ala	Val	Ser	Leu	Pro	Ser	Phe	Phe	Asn
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Val	Ile	Pro	His	Ala	Asn	Gly	Leu	Glu	Gln	Ile	Ser	Gly	Gly	Asp	Thr
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Asn	Met	Phe	Arg	Leu	Ala	Lys	Glu	Gln	Gly	Tyr	Glu	Thr	Tyr	Phe	Tyr
	290					295					300				
Ser	Ala	Gln	Ala	Glu	Asn	Gln	Met	Ala	Ile	Leu	Asn	Leu	Ile	Gly	Lys
305					310					315					320
Lys	Trp	Ile	Asp	His	Leu	Ile	Gln	Pro	Thr	Gln	Leu	Gly	Tyr	Gly	Asn
				325					330					335	
Gly	Asp	Asn	Met	Pro	Asp	Glu	Lys	Leu	Leu	Pro	Leu	Phe	Asp	Lys	Ile
			340					345					350		
Asn	Leu	Gln	Gln	Gly	Arg	His	Phe	Ile	Val	Leu	His	Gln	Arg	Gly	Ser
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His	Ala	Pro	Tyr	Gly	Ala	Leu	Leu	Gln	Pro	Gln	Asp	Lys	Val	Phe	Gly
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Glu	Ala	Asp	Ile	Val	Asp	Lys	Tyr	Asp	Asn	Thr	Ile	His	Lys	Thr	Asp
385					390					395					400
Gln	Met	Ile	Gln	Thr	Val	Phe	Glu	Gln	Leu	Gln	Lys	Gln	Pro	Asp	Gly
			405					410						415	
Asn	Trp	Leu	Phe	Ala	Tyr	Thr	Ser	Asp	His	Gly	Gln	Tyr	Val	Arg	Gln
		420						425					430		
Asp	Ile	Tyr	Asn	Gln	Gly	Thr	Val	Gln	Pro	Asp	Ser	Tyr	Ile	Val	Pro
	435						440					445			
Leu	Val	Leu	Tyr	Ser	Pro	Asp	Lys	Ala	Val	Gln	Gln	Ala	Ala	Asn	Gln
	450						455					460			
Ala	Phe	Ala	Pro	Cys	Glu	Ile	Ala	Phe	His	Gln	Gln	Leu	Ser	Thr	Phe
465					470					475					480
Leu	Ile	His	Thr	Leu	Gly	Tyr	Asp	Met	Pro	Val	Ser	Gly	Cys	Arg	Glu
				485					490					495	
Gly	Ser	Val	Thr	Gly	Asn	Leu	Ile	Thr	Gly	Asp	Ala	Gly	Ser	Leu	Asn
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Ile	Arg	Asn	Gly	Lys	Ala	Glu	Tyr	Val	Tyr	Pro	Gln				
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1 5 10 15

ttg ctg acg gaa aaa gtg tgc ccc atc atc gca tta atc ttg gtg ccg 96
Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro
20 25 30

ctg att ggg gcg ttg ctg gcg ggg ttt gat gta tcc caa tta aaa gaa 144
Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu
35 40 45

ttt tat tgc ggc ggc acg aaa tgc gtg acg cag att gtg att atg ttt 192
Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe
50 55 60

atg ttt tcc att ttg ttt ttt gga atc atg aac gat gtg ggg ctg ttc 240
Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe
65 70 75 80

cgt ccg atg ata ggc ggt ttg att aag ctg act cgg ggt aat atc gtg 288
Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val
85 90 95

gca gtg agt gtg ggg acg gtc ttg gtg tgc gtg gtg gca cag ttg gac 336
Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp
100 105 110

ggg gcg ggc gcg acg acg ttt tta tgc gtc gtc ccc gcc ctt ttg ccg 384
Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro
115 120 125

ctt tac aag cgt ctg cat atg aat cct tac ctg ctg ttt ttg ctg ctg 432
Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu
130 135 140

act tcc agc gcg ggg cta atc aac ctt ttg ccg cgg ggc ggg ccg atc 480
Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile
145 150 155 160

ggg cgg gtt gca agc gtg ttg ggc gca gat gtg ggc gaa ttg tat aaa 528
Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys
165 170 175

cct ttg ttg acg gtg caa att atc ggt gtg gtg ttt atc ctt gtg ctg 576
Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Val Leu
180 185 190

tcc ctg ttt ttg ggt gtg cgt gaa aaa agg cgg att gtc cgg gag ttg 624
Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu
195 200 205

ggc gcg ttg ccc gcc gtg gcg gat ttg ata aag ccg gcg cct ttg tgc 672
Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser
210 215 220

gaa gaa gaa caa aaa ttg gcg cgt ccg aaa ctg ttt tgg tgg aat gtc 720
Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val

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Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu
 35 40 45
 Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe
 50 55 60
 Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe
 65 70 75 80
 Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val
 85 90 95
 Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp
 100 105 110
 Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro
 115 120 125
 Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu
 130 135 140
 Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile
 145 150 155 160
 Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys
 165 170 175
 Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Val Leu
 180 185 190
 Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu
 195 200 205
 Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser
 210 215 220
 Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val
 225 230 235 240
 Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro
 245 250 255
 Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn
 260 265 270
 Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly
 275 280 285
 Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu
 290 295 300
 Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu
 305 310 315 320
 Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile
 325 330 335
 Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr
 340 345 350
 Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly
 355 360 365
 Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val
 370 375 380

009130-001504

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly
385 390 395 400

Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp
405 410 415

Ala Trp Gly Leu Ser Leu Ala Ile Leu Val Ser Ser Ile Ala Ala Gly
420 425 430

Ile Val Pro Leu Pro
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<213> Neisseria gonorrhoeae

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act tat ctg tat caa aag ccc aag ctc ttt aaa gga gcg gtt cgg aat 96
Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn
20 25 30
ctc gaa gcc gca tct tgt aaa tat atc aac gag ata tac caa cga gca 144
Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala
35 40 45
gac cca acc gca ccg ctg ttt cat ctg cgt aaa aaa ggc gca atc gtt 192
Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val
50 55 60
cct aaa gaa gaa tac gtc gaa agt ttc gac gat ttg ggc aaa act cgc 240
Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg
65 70 75 80
tac cgt ttt att aaa tcc gtt atc tac gaa cat atg aag aat ggt gcg 288
Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala
85 90 95
tcg tta gtc tat aac cat att aac aac gag ccg ttt tca gac cat atc 336
Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile
100 105 110
gcc cgt caa gtc gcc cgc ttt gcc ggc gca cat act att gtt agt gga 384
Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly
115 120 125
tat ctt gct ttt ggc agc gac gaa tct tat aaa aac cat tgg gat acc 432
Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr
130 135 140
cgc gat gtg tat gcc atc cag ctt ttc ggc aag aaa cgt tgg caa ctt 480
Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu
145 150 155 160
act gcc cct gat ttc cct atg cca ttg tat atg caa cag act aaa gat 528

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Thr	Asp	Ile	Ser	Ile	Pro	Glu	His	Ile	Asp	Met	Asp	Ile	Ile	Leu	Glu		
			180					185					190				
gca	ggt	gat	gtc	ctc	tac	atc	cca	cgc	ggt	tgg	tgg	cac	aga	cct	atc	624	
Ala	Gly	Asp	Val	Leu	Tyr	Ile	Pro	Arg	Gly	Trp	Trp	His	Arg	Pro	Ile		
			195				200					205					
ccg	ctc	ggc	tgt	gaa	acc	ttc	cac	ttc	gct	gtc	ggt	acc	ttc	cca	cca	672	
Pro	Leu	Gly	Cys	Glu	Thr	Phe	His	Phe	Ala	Val	Gly	Thr	Phe	Pro	Pro		
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Asn	Gly	Tyr	Asn	Tyr	Leu	Glu	Trp	Leu	Met	Lys	Lys	Phe	Pro	Thr	Ile		
225					230				235						240		
gaa	agt	ctg	cgc	cac	agt	ttc	tca	gac	tgg	gag	caa	gat	agg	acg	cgt	768	
Glu	Ser	Leu	Arg	His	Ser	Phe	Ser	Asp	Trp	Glu	Gln	Asp	Arg	Thr	Arg		
				245					250					255			
atc	aac	gat	act	gcc	gca	caa	att	gct	gcc	atg	att	gcc	gac	ccc	gtc	816	
Ile	Asn	Asp	Thr	Ala	Ala	Gln	Ile	Ala	Ala	Met	Ile	Ala	Asp	Pro	Val		
			260					265					270				
aat	tat	gaa	gcc	ttc	agt	gaa	gac	ttt	ctc	ggc	aaa	gaa	cgt	acc	gat	864	
Asn	Tyr	Glu	Ala	Phe	Ser	Glu	Asp	Phe	Leu	Gly	Lys	Glu	Arg	Thr	Asp		
		275					280					285					
acc	gct	ttt	cat	ctc	gaa	cag	ttc	gcg	aat	ccc	aac	gct	act	ccg	ctt	912	
Thr	Ala	Phe	His	Leu	Glu	Gln	Phe	Ala	Asn	Pro	Asn	Ala	Thr	Pro	Leu		
	290					295					300						
tca	gac	gac	gtc	agg	ttg	aga	tta	aat	gcc	aat	aat	ttg	gat	acg	ttg	960	
Ser	Asp	Asp	Val	Arg	Leu	Arg	Leu	Asn	Ala	Asn	Asn	Leu	Asp	Thr	Leu		
305					310				315						320		
gaa	aag	gga	tat	ttg	att	ggg	aat	ggg	atg	aag	ata	agc	gta	gat	gag	1008	
Glu	Lys	Gly	Tyr	Leu	Ile	Gly	Asn	Gly	Met	Lys	Ile	Ser	Val	Asp	Glu		
				325				330						335			
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Leu	Gly	Lys	Lys	Val	Leu	Glu	His	Ile	Gly	Lys	Asn	Glu	Pro	Leu	Leu		
			340					345					350				
ttg	aaa	aat	cta	ctg	gtt	aac	ttc	aat	cag	gca	aaa	cat	gaa	gaa	gtt	1104	
Leu	Lys	Asn	Leu	Leu	Val	Asn	Phe	Asn	Gln	Ala	Lys	His	Glu	Glu	Val		
		355					360					365					
agg	aag	ttg	atc	tat	cag	ttg	ata	gag	tta	gat	ttt	ctg	gaa	att	ttg	1152	
Arg	Lys	Leu	Ile	Tyr	Gln	Leu	Ile	Glu	Leu	Asp	Phe	Leu	Glu	Ile	Leu		
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Leu	Glu	Ala 35	Ala	Ser	Cys	Lys	Tyr 40	Ile	Asn	Glu	Ile	Tyr 45	Gln	Arg	Ala
Asp	Pro 50	Thr	Ala	Pro	Leu	Phe 55	His	Leu	Arg	Lys	Lys 60	Gly	Ala	Ile	Val
Pro 65	Lys	Glu	Glu	Tyr	Val 70	Glu	Ser	Phe	Asp	Asp 75	Leu	Gly	Lys	Thr	Arg 80
Tyr	Arg	Phe	Ile	Lys 85	Ser	Val	Ile	Tyr	Glu 90	His	Met	Lys	Asn	Gly 95	Ala
Ser	Leu	Val	Tyr 100	Asn	His	Ile	Asn 105	Asn	Glu	Pro	Phe	Ser	Asp 110	His	Ile
Ala	Arg	Gln 115	Val	Ala	Arg	Phe	Ala 120	Gly	Ala	His	Thr	Ile 125	Val	Ser	Gly
Tyr	Leu 130	Ala	Phe	Gly	Ser	Asp 135	Glu	Ser	Tyr	Lys	Asn 140	His	Trp	Asp	Thr
Arg 145	Asp	Val	Tyr	Ala	Ile 150	Gln	Leu	Phe	Gly	Lys 155	Lys	Arg	Trp	Gln	Leu 160
Thr	Ala	Pro	Asp	Phe 165	Pro	Met	Pro	Leu	Tyr 170	Met	Gln	Gln	Thr	Lys 175	Asp
Thr	Asp	Ile	Ser 180	Ile	Pro	Glu	His	Ile 185	Asp	Met	Asp	Ile	Ile 190	Leu	Glu
Ala	Gly	Asp 195	Val	Leu	Tyr	Ile	Pro 200	Arg	Gly	Trp	Trp	His 205	Arg	Pro	Ile
Pro 210	Leu	Gly	Cys	Glu	Thr	Phe 215	His	Phe	Ala	Val	Gly 220	Thr	Phe	Pro	Pro
Asn 225	Gly	Tyr	Asn	Tyr	Leu 230	Glu	Trp	Leu	Met	Lys 235	Lys	Phe	Pro	Thr	Ile 240
Glu	Ser	Leu	Arg	His 245	Ser	Phe	Ser	Asp	Trp 250	Glu	Gln	Asp	Arg	Thr 255	Arg
Ile	Asn	Asp	Thr 260	Ala	Ala	Gln	Ile	Ala 265	Ala	Met	Ile	Ala	Asp 270	Pro	Val
Asn	Tyr	Glu 275	Ala	Phe	Ser	Glu	Asp 280	Phe	Leu	Gly	Lys	Glu 285	Arg	Thr	Asp
Thr	Ala 290	Phe	His	Leu	Glu	Gln 295	Phe	Ala	Asn	Pro	Asn 300	Ala	Thr	Pro	Leu
Ser 305	Asp	Asp	Val	Arg	Leu 310	Arg	Leu	Asn	Ala	Asn 315	Asn	Leu	Asp	Thr	Leu 320
Glu	Lys	Gly	Tyr	Leu 325	Ile	Gly	Asn	Gly	Met 330	Lys	Ile	Ser	Val	Asp 335	Glu
Leu	Gly	Lys	Lys 340	Val	Leu	Glu	His	Ile 345	Gly	Lys	Asn	Glu	Pro 350	Leu	Leu
Leu	Lys	Asn 355	Leu	Leu	Val	Asn	Phe 360	Asn	Gln	Ala	Lys	His 365	Glu	Glu	Val

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Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile
210 215 220

cgc acg cag aat ctg aca ttg gcc agc ctc ccc caa gcg gca tga 717
Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala
225 230 235

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<212> PRT
<213> Neisseria meningitidis
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Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile
35 40 45

Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly
50 55 60

Gln Ile_Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr
65 - 70 75 80

Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala
85 90 95

Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp
100 105 110

Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu
 . 115 120 125

Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr
130 135 140

Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Glu Leu His
145 150 155 160

Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu
165 170 175

Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro
180 185 190

Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala
195 200 205

Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile
210 215 220

Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala
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gcc tac ggc cga gaa gaa gcc ggg ctg ctt cag gaa atc cgc acg cag 96
 Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln
 20 25 30

aat ctg aca ttg gcc agc ctc ccc aaa cgg cat gag aca gaa caa agc 144
 Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
 35 40 45

cag ctt gaa cgc acc atg gcc gat att tct caa gaa gtt ttg gat ttt 192
 Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
 50 55 60

gaa atg cgc tct gaa caa atc atc cgt gca gga cgg tcg ggt tat ata 240
 Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
 65 70 75 80

gca ata ccg aac gtc gaa gtc gga cgg cag gtt gat cct tcc aaa ctg 288
 Ala Ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu
 85 90 95

ctc ttg agc att gtt ccc gaa cgt acc gag tta tat gcc cat cta tat 336
 Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr
 100 105 110

atc ccc agc agt gca gca ggc ttt atc aag ccg aaa gac aag gtt gtc 384
 Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val
 115 120 125

cta cgt tat cag gca tat ccc tat cag aaa ttc ggg ctt gct tcc ggc 432
 Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
 130 135 140

agt gtc gta tca gtg gca aaa acg gca ctg ggc aga cag gaa ttg tcg 480
 Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
 145 150 155 160

gga ttg ggc atg gta tcc tcc gat ttg gcg aag agc aac gaa cct gtt 528
 Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
 165 170 175

tat ctc gtg aaa ata aaa ccc gac aaa cca acc atc act gca tac ggt 576
 Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
 180 185 190

gag gaa aaa ccg ctg caa atc ggc atg acg ctg gaa gca gac atc cta 624
 Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
 195 200 205

cac gag aaa cgg cgg ctg tac gaa tgg gta ttg gag ccg att tac agt 672
 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser
 210 215 220

atg tcg ggc agg ttg taa 690
 Met Ser Gly Arg Leu

103730 "03403860"

atg	caa	tac	agc	aca	ctg	gca	gga	caa	acc	gac	aac	tcc	ctc	gtt	tcc	48
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Asn	Asn	Phe	Gly	Phe	Leu	Arg	Leu	Pro	Leu	Asn	Phe	Met	Pro	Tyr	Glu	
			20					25					30			
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Ser	His	Ala	Asp	Trp	Val	Ile	Thr	Gly	Val	Pro	Tyr	Asp	Met	Ala	Val	
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Ser	Gly	Arg	Ser	Gly	Ala	Arg	Phe	Gly	Pro	Glu	Ala	Ile	Arg	Arg	Ala	
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Ser	Val	Asn	Leu	Ala	Trp	Glu	His	Arg	Arg	Phe	Pro	Trp	Thr	Phe	Asp	
	65				70				75						80	
gtg	cgc	gaa	cgc	ctg	aac	att	att	gat	tgc	ggc	gac	ttg	gtt	ttt	tct	288
Val	Arg	Glu	Arg	Leu	Asn	Ile	Ile	Asp	Cys	Gly	Asp	Leu	Val	Phe	Ser	
				85				90						95		
ttt	ggc	gac	agc	agg	gat	ttt	gtc	gaa	aaa	atg	gaa	gcg	cac	gcc	ggc	336
Phe	Gly	Asp	Ser	Arg	Asp	Phe	Val	Glu	Lys	Met	Glu	Ala	His	Ala	Gly	
			100					105					110			
aaa	tta	ctt	tct	ttc	ggc	aaa	cgc	tgt	ttg	agt	ttg	ggc	ggc	gac	cat	384
Lys	Leu	Leu	Ser	Phe	Gly	Lys	Arg	Cys	Leu	Ser	Leu	Gly	Gly	Asp	His	
		115					120					125				
ttc	att	acc	ctc	ccg	ttg	ttg	cgc	gcc	cac	gcc	cgc	tat	ttc	ggc	aaa	432
Phe	Ile	Thr	Leu	Pro	Leu	Leu	Arg	Ala	His	Ala	Arg	Tyr	Phe	Gly	Lys	
	130					135					140					
ctc	gca	ctg	att	cat	ttt	gac	gcg	cac	acc	gac	acc	tac	gac	aac	ggc	480
Leu	Ala	Leu	Ile	His	Phe	Asp	Ala	His	Thr	Asp	Thr	Tyr	Asp	Asn	Gly	
	145				150					155					160	
agc	gaa	tac	gac	cac	ggc	acg	atg	ttt	tat	acc	gcc	ccc	aag	gaa	ggc	528
Ser	Glu	Tyr	Asp	His	Gly	Thr	Met	Phe	Tyr	Thr	Ala	Pro	Lys	Glu	Gly	
				165				170						175		
ctc	atc	gac	ccg	tcc	cgt	tcc	gta	caa	atc	ggc	ata	cgc	acc	gaa	cac	576
Leu	Ile	Asp	Pro	Ser	Arg	Ser	Val	Gln	Ile	Gly	Ile	Arg	Thr	Glu	His	
			180					185					190			
agt	aaa	aaa	ttg	cct	ttt	act	gtg	ttg	tcc	gcc	ccc	aaa	gtc	aat	gaa	624
Ser	Lys	Lys	Leu	Pro	Phe	Thr	Val	Leu	Ser	Ala	Pro	Lys	Val	Asn	Glu	
	195						200					205				
gac	agt	gtt	gaa	gag	acc	gtc	cgt	aaa	atc	aaa	gaa	acc	gtc	ggc	aat	672
Asp	Ser	Val	Glu	Glu	Thr	Val	Arg	Lys	Ile	Lys	Glu	Thr	Val	Gly	Asn	
	210					215					220					
atg	ccc	gtt	tac	ctg	act	ttc	gac	ata	gac	tgt	ctc	gac	ccg	tcg	ttc	720
Met	Pro	Val	Tyr	Leu	Thr	Phe	Asp	Ile	Asp	Cys	Leu	Asp	Pro	Ser	Phe	
	225				230				235						240	
gcc	ccc	ggg	acc	ggg	acg	ccc	gta	tgc	ggc	ggc	ttg	agc	agc	gac	agg	768
Ala	Pro	Gly	Thr	Gly	Thr	Pro	Val	Cys	Gly	Gly	Leu	Ser	Ser	Asp	Arg	
				245				250						255		
gca	tta	aaa	atc	cta	cgt	ggg	ctg	acg	gat	ctc	gac	atc	gtc	ggg	atg	816
Ala	Leu	Lys	Ile	Leu	Arg	Gly	Leu	Thr	Asp	Leu	Asp	Ile	Val	Gly	Met	

260

265

270

gat gtt gta gaa gtt gcc ccc tct tac gac caa tcc gac att acc gct 864
 Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
 275 280 285

ttg gcc ggc gcc aca att gcc ttg gaa atg ctt tac ctt caa ggt gcg 912
 Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala
 290 295 300

aaa aag gac tga 924
 Lys Lys Asp
 305

<210> 67

<211> 307

<212> PRT

<213> Neisseria gonorrhoeae

<400> 67

Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser
 1 5 10 15

Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu
 20 25 30

Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val
 35 40 45

Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
 50 55 60

Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
 65 70 75 80

Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
 85 90 95

Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly
 100 105 110

Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His
 115 120 125

Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys
 130 135 140

Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly
 145 150 155 160

Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly
 165 170 175

Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His
 180 185 190

Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu
 195 200 205

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
 210 215 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
 225 230 235 240

0533043-031601

ctg ttg aaa gtt gcc gaa agt tat ttc aac gtt tta ctc agc cga gac	528
Leu Leu Lys Val Ala' Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp	
165 170 175	
acc gtt gcc gcc cat gcg gcg gaa aaa gag gct tat gcc cag cag gta	576
Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val	
180 185 190	
agg cag gcg cag gct tta ttc aat aaa ggt gct gcc acc gcg ctg gat	624
Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp	
195 200 205	
att cac gaa gcc aaa gcc ggt tac gac aat gcc ctg gcc caa gaa atc	672
Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile	
210 215 220	
gcc gta ttg gct gag aaa caa acc tat gaa aac cag ttg aac gac tac	720
Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr	
225 230 235 240	
acc gac ctg gat agc aaa caa atc gag gcc ata gat acc gcc aac ctg	768
Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu	
245 250 255	
ttg gca cgc tat ctg ccc aag ctg gaa cgt tac agt ctg gat gaa tgg	816
Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp	
260 265 270	
cag cgc att gcc tta tcc aac aat cat gaa tac cgg atg cag cag ctt	864
Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu	
275 280 285	
gcc ctg caa agc agc gga cag gcg ctt cgg gca gca cag aac agc cgc	912
Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg	
290 295 300	
tat ccc acc gtt tct gcc cat gtc ggc tat cag aat aac ctc tac act	960
Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr	
305 310 315 320	
tca tct gcg cag aat aat gac tac cac tat cgg ggc aaa ggg atg agc	1008
Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser	
325 330 335	
gtc ggc gta cag ttg aat ttg ccg ctt tat acc ggc gga gaa ttg tcg	1056
Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser	
340 345 350	
ggc aaa atc cat gaa gcc gaa gcg caa tac ggg gcc gcc gaa gca cag	1104
Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln	
355 360 365	
ctg acc gca acc gag cgg cac atc aaa ctc gcc gta cgc cag gct tat	1152
Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr	
370 375 380	
acc gaa agc ggt gcg gcg cgt tac caa atc atg gcg caa gaa cgg gtt	1200
Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val	
385 390 395 400	
ttg gaa agc agc cgt ttg aaa ctg aaa tcg acc gaa acc ggc caa caa	1248
Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln	
405 410 415	
tac ggc atc cgc aac cgg ctg gaa gta ata cgg gcg cgg cag gaa gtc	1296

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
420 425 430

gcc caa gca gaa cag aaa ctg gct caa gca cgg tat aaa ttc atg ctg 1344
Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
435 440 445

gct tat ttg cgc ttg gtg aaa gag agc ggg tta ggg ttg gaa acg gta 1392
Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
450 455 460

ttt gcg gaa taa 1404
Phe Ala Glu
465

<210> 69

<211> 467

<212> PRT

<213> Neisseria meningitidis

<400> 69

Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
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Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
20 25 30

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
35 40 45

Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
50 55 60

Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
65 70 75 80

Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
85 90 95

Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
100 105 110

Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln
115 120 125

Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe
130 135 140

Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu
145 150 155 160

Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp
165 170 175

Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val
180 185 190

Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp
195 200 205

Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile
210 215 220

Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr
225 230 235 240

09830433-081604

Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu
245' 250 255

Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp
260 265 270

Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu
275 280 285

Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Gln Asn Ser Arg
290 295 300

Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr
305 310 315 320

Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser
325 330 335

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
450 455 460

Phe Ala Glu
465

<210> 70
<211> 696
<212> DNA
<213> Neisseria gonorrhoeae

<220>
<221> CDS
<222> (1)..(693)

<400> 70
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Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn
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aca ttg ggc att tgc gcg ctt tta gcc ttt tgt ttt ggc gcg gcc atc 96
Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
20 25 30

gca tca ggt tat cac ttg gaa tat gaa tac ggc tac cgt tat tct gcc	144
Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala	
35 40 45	
gtg ggc gct ttg gct tcg gtt gta ttt tta tta tta ttg gca cgc ggc	192
Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly	
50 55 60	
ttc ccg cgc gtt tct tca gtt gtt tta ctg att tac gtc ggc aca acc	240
Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr	
65 70 75 80	
gcc cta tat ttg ccg gtc ggc tgg ctg tat ggt gcg cct tct tat cag	288
Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln	
85 90 95	
ata gtc ggt tcg ata ttg gaa agc aat cct gcc gag gcg cgt gaa ttt	336
Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe	
100 105 110	
gtc ggc aat ctt ccc ggg tcg ctt tat ttt gtg cag gca tta ttt ttc	384
Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe	
115 120 125	
att ttt ggc ttg aca gtt tgg aaa tat tgt gta tct gtg ggg gta ttt	432
Ile Phe Gly Leu Thr Val Trp Lys Tyr Cys Val Ser Val Gly Val Phe	
130 135 140	
gct gac gta aaa aac tat aaa cgt cgc agc aaa ata tgg ctg acc ata	480
Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile	
145 150 155 160	
tta ttg act ttg att ttg tcc tgc gcg gtg atg gag aaa atc gcc ggc	528
Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Glu Lys Ile Ala Gly	
165 170 175	
gat aaa gat tgg cga gaa cct gat gcc ggc ctg ttg ttg aat att ttc	576
Asp Lys Asp Trp Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe	
180 185 190	
gac ctg tat tac gac ttg gct ttc cgc gcc ggc aca ata tgc cgc caa	624
Asp Leu Tyr Tyr Asp Leu Ala Phe Arg Ala Gly Thr Ile Cys Arg Gln	
195 200 205	
gcg cgc cca cat ttt gga agc agc aaa aaa agc gtc aac atg gca tat	672
Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr	
210 215 220	
ccg cca act tgc gcc caa gta taa	696
Pro Pro Thr Cys Ala Gln Val	
225 230	

<210> 71

<211> 231

<212> PRT

<213> Neisseria gonorrhoeae

<400> 71

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1				5					10					15	

Thr	Leu	Gly	Ile	Cys	Ala	Leu	Leu	Ala	Phe	Cys	Phe	Gly	Ala	Ala	Ile
			20					25					30		

Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala

Val Gly Ala Leu Ala' Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly
 50 55 60

Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr
 65 70 75 80

Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln
 85 90 95

Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe
 100 105 110

Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe
 115 120 125

Ile Phe Gly Leu Thr Val Trp Lys Tyr Cys Val Ser Val Gly Val Phe
 130 135 140

Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile
 145 150 155 160

Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Glu Lys Ile Ala Gly
 165 170 175

Asp Lys Asp Trp Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe
 180 185 190

Asp Leu Tyr Tyr Asp Leu Ala Phe Arg Ala Gly Thr Ile Cys Arg Gln
 195 200 205

Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr
 210 215 220

Pro Pro Thr Cys Ala Gln Val
 225 230

<210> 72

<211> 2607

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1)..(2604)

<400> 72

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 1 5 10 15

gaa tac tac gac gcg cgt gcg gcg tgt gag ggc atc aaa ccc ggc tct 96

Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Gly Ile Lys Pro Gly Ser
 20 25 30

tac gac aag ctg cct tac acg agc cgc att ttg gcg gag aat ttg gtc 144

Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
 35 40 45

aac cgc gcg gac aaa gtc gat ttg ccg acg ctg caa agc tgg ctg ggt 192

Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
 50 55 60

T09T30"EE40E860

cag ctg att gag gga aaa cag gaa atc gac ttt cct tgg tat ccg gcg Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala 65 70 75 80	240
cggtgtgtgtgcacgatattctggggcagaccgcgttggtgatttg Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu 85 90 95	288
gca ggt ctg cgc gat gcg att gcc gaa aaa ggc ggc gat cct gcc aaa Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys 100 105 110	336
gtg aat ccg gtg gtg caa acc cag ctc atc gtc gac cac tcg ctg gcg Val Asn Pro Val Val Gln Thr Gln Leu Ile Val Asp His Ser Leu Ala 115 120 125	384
gtg gaa tgc ggc ggc tac gac ccc gat gcg ttc cgc aaa aac cgc gaa Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu 130 135 140	432
atc gaa gac aga cgt aac gaa gac cgt ttc cac ttc atc aac tgg aca Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr 145 150 155 160	480
aaa acc gct ttt gaa aat gtg gac gtg att ccg gcg ggc aac ggc atc Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly Ile 165 170 175	528
atg cac caa atc aat cta gaa aaa atg tcg ccc gtc gtc caa gtc aaa Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys 180 185 190	576
aac ggc gtg gct ttc ccc gat acc tgc gtc ggc acg gat tcg cac acg Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr 195 200 205	624
cca cac gtc gat gcg ctg ggc gtg att tcc gtg ggc gtg ggc gga ttg Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly Leu 210 215 220	672
gaa gcg gaa acc gta atg ctg gga cgc gcg tcc atg atg cgc ctg ccc Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro 225 230 235 240	720
gat att gtc ggc gtt gag ctg aac ggc aaa cgg aag gcg ggc att acg Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr 245 250 255	768
gcg acg gat att gtg ttg gca ctg acc gag ttt ctg cgc aaa gaa cgc Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu Arg 260 265 270	816
gtg gtc ggg gcg ttt gtc gaa ttc ttc ggc gag ggc gcg aga agc ctg Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser Leu 275 280 285	864
tct atc ggc gac cgc gcg acc att tcc aac atg acg ccg gag ttc ggc Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly 290 295 300	912
gcg act gcc gcg atg ttc gct att gat gag caa acc att gat tat ttg Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr Leu 305 310 315 320	960
aaa ctg acc gga cgc gac gac gcg cag gtg aaa ttg gtg gaa acc tac Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr Tyr	1008

gcc aaa acc gca ggc' ttg tgg gca gat gcc ttg aaa acc gcc gtt tat	1056
Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val Tyr	
340 345 350	
ccg cgc gtt ttg aaa ttt gat ttg agc agc gta acg cgc aat atg gca	1104
Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met Ala	
355 360 365	
ggc ccg agc aac ccg cac gcg cgt ttt gcg acc gcc gat ttg gcc ggc	1152
Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly	
370 375 380	
aaa ggc ttg gct aaa cct tac gaa gag cct tca gac ggc caa atg cct	1200
Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met Pro	
385 390 395 400	
gac ggt gca gtg att att gcc gcg att act tcc tgt acc aat act tcc	1248
Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser	
405 410 415	
aat ccg cgc aac gtt gtc gcc gcc gcg ctg ttg gca cgc aat gcc aac	1296
Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala Asn	
420 425 430	
cgc ctc ggc ttg caa cgc aaa cct tgg gtg aaa tct tcg ttt gcc ccg	1344
Arg Leu Gly Leu Gln Arg Lys Pro Trp Val Lys Ser Ser Phe Ala Pro	
435 440 445	
ggt tca aaa gta gcc gaa atc tat ttg aaa gaa gca gat ctg ctg ccc	1392
Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Asp Leu Leu Pro	
450 455 460	
gaa atg gaa aaa ctc ggc ttc ggt atc gtt gcc ttc gca tgt acc acc	1440
Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr Thr	
465 470 475 480	
tgt aac ggc atg agc ggc gcg ctg gat ccg aaa atc cag aaa gaa atc	1488
Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu Ile	
485 490 495	
atc gac cgc gat ttg tac gcc acc gcc gta ttg tca ggc aac cgc aac	1536
Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg Asn	
500 505 510	
ttt gac ggc cgt atc cat ccg tat gcg aaa cag gct ttc ctc gct tcg	1584
Phe Asp Gly Arg Ile His Pro Tyr Ala Lys Gln Ala Phe Leu Ala Ser	
515 520 525	
cct ccg ttg gtc gtt gcc tac gcg ctg gca ggc agc atc cgt ttc gat	1632
Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe Asp	
530 535 540	
att gaa aac gac gta ctc ggc gtt gca gac ggc aaa gaa atc cgc ctg	1680
Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg Leu	
545 550 555 560	
aaa gac att tgg cct acc gat gaa gaa atc gat gcc atc gtt gcc gaa	1728
Lys Asp Ile Trp Pro Thr Asp Glu Glu Ile Asp Ala Ile Val Ala Glu	
565 570 575	
tat gtg aaa ccg cag caa ttt cgc gac gtt tat atc ccg atg ttc gac	1776
Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Ile Pro Met Phe Asp	
580 585 590	

T09720" E40E360

acc ggc aca gcg caa aaa gca cca agc ccg ctg tac gac tgg cgt cca	1824
Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg Pro	
595 , , 600 605	
atg tct acc tat atc cgc cgc cca cct tac tgg gaa ggc gca ctg gca	1872
Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala	
610 615 620	
ggg gaa cgc aca tta agc ggt atg cgt ccg ctg gcg att ttg ccc gac	1920
Gly Glu Arg Thr Leu Ser Gly Met Arg Pro Leu Ala Ile Leu Pro Asp	
625 630 635 640	
aac atc acc acc gac cat ctc tcg cca tcc aat gcg att ttg gca agc	1968
Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala Ser	
645 650 655	
agt gcc gca ggc gaa tat ttg gca aaa atg ggt ttg cct gaa gaa gac	2016
Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu Asp	
660 665 670	
ttc aac tct tac gca acc cac cgt ggc gac cac ttg acc gcc caa cgc	2064
Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln Arg	
675 680 685	
gca acc ttc gcc aat ccg aaa ctg ttt aac gaa atg gtg aga aac gaa	2112
Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Arg Asn Glu	
690 695 700	
gac ggc agc gta cgc caa ggt tcg ctg gca cgc gtt gaa ccc gaa ggc	2160
Asp Gly Ser Val Arg Gln Gly Ser Leu Ala Arg Val Glu Pro Glu Gly	
705 710 715 720	
caa acc atg cgc atg tgg gaa gcc atc gaa acc tat atg aac cgc aaa	2208
Gln Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg Lys	
725 730 735	
cag ccg ctc atc atc att gcc ggc gcg gac tac ggt caa ggc tca agc	2256
Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser Ser	
740 745 750	
cgc gac tgg gct gca aaa ggc gta cgc ctc gcc ggc gtg gaa gcg att	2304
Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala Ile	
755 760 765	
gtt gcc gaa ggc ttc gag cgt atc cac cgc acc aac ttg atc ggt atg	2352
Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met	
770 775 780	
ggc gtg ttg ccg ctg cag ttc aaa ccg ggt acc aac cgc cac acc ctg	2400
Gly Val Leu Pro Leu Gln Phe Lys Pro Gly Thr Asn Arg His Thr Leu	
785 790 795 800	
caa ctg gac ggt acg gaa acc tac gac gtt gtc ggc gaa cgc aca ccg	2448
Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro	
805 810 815	
cgc tgc gac ctg acc ctt gtg att cac cgt aaa aac ggc gag acc gtc	2496
Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val	
820 825 830	
gaa gtc ccc att acc tgc cgc ctc gat acc gca gaa gaa gtg ttg gta	2544
Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val	
835 840 845	
tat gaa gcc ggt ggc gta ttg caa cgg ttt gca cag gat ttt ttg gaa	2592
Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu Glu	

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ggg aac gcg gct tag⁺
Gly Asn Ala Ala
865

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<210> 73
<211> 868
<212> PRT
<213> Neisseria meningitidis
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<400> 73

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Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Gly Ile Lys Pro Gly Ser
20 25 30

Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
35 40 45

Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
50 55 60

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
65 70 75 80

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu .
 85 90 95

Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys
100 105 110

Val	Asn	Pro	Val	Val	Gln	Thr	Gln	Leu	Ile	Val	Asp	His	Ser	Leu	Ala
		115					120					125			

Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu
130 135 140

Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr
145 150 155 160

Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly Ile
165 170 175

Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys
180 185 190

Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr
195 200 205

Pro	His	Val	Asp	Ala	Leu	Gly	Val	Ile	Ser	Val	Gly	Val	Gly	Gly	Leu
210						215					220				

Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro
225 230 235 240

Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr
245 250 255

Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu Arg
260 265 270

Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser Leu
275 280 285[illegible]

Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly
 290 295 300
 Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr Leu
 305 310 315 320
 Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr Tyr
 325 330 335
 Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val Tyr
 340 345 350
 Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met Ala
 355 360 365
 Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly
 370 375 380
 Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met Pro
 385 390 395 400
 Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser
 405 410 415
 Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala Asn
 420 425 430
 Arg Leu Gly Leu Gln Arg Lys Pro Trp Val Lys Ser Ser Phe Ala Pro
 435 440 445
 Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Asp Leu Leu Pro
 450 455 460
 Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr Thr
 465 470 475 480
 Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu Ile
 485 490 495
 Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg Asn
 500 505 510
 Phe Asp Gly Arg Ile His Pro Tyr Ala Lys Gln Ala Phe Leu Ala Ser
 515 520 525
 Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe Asp
 530 535 540
 Ile Glu Asn Asp Val Leu Gly Val Ala Asp Gly Lys Glu Ile Arg Leu
 545 550 555 560
 Lys Asp Ile Trp Pro Thr Asp Glu Glu Ile Asp Ala Ile Val Ala Glu
 565 570 575
 Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Ile Pro Met Phe Asp
 580 585 590
 Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg Pro
 595 600 605
 Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala
 610 615 620
 Gly Glu Arg Thr Leu Ser Gly Met Arg Pro Leu Ala Ile Leu Pro Asp
 625 630 635 640

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gcg gga agc gca cgc gac aaa atc ctc ttg cgc gta ctc ggc agc ccg Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro 35 40 45	144
gat ccc tac ggc aag cag ata gac ggt ttg ggc aac gcc agc tcg tcc Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser 50 55 60	192
acc agc aag gcg gtg att ttg gac aag tcc gaa cgc gcc gat cac gat Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp 65 70 75 80	240
gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa cct ttt gtc gat Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp 85 90 95	288
tgg agt ggc aac tgc ggc aac ctc acc gcc gcc gtg ggc gca ttt gcc Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala 100 105 110	336
atc gag caa ggc ttg gtc gat aaa ggc aag att cct tca gac ggc atc Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile 115 120 125	384
tgc aca gtc aaa atc tgg cag aaa aac atc ggc aaa acc att att gcc Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala 130 135 140	432
cat gta ccg atg caa aac ggc gca gtt ttg gaa aca ggc gat ttt gag His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu 145 150 155 160	480
ctc gac ggc gta acg ttc ccg gca gcc gaa gta caa atc gaa ttt ctt Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu 165 170 175	528
gat cca gcc gac ggc gaa ggc agt atg ttc cca acc ggc aat ttg gtc Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val 180 185 190	576
gat gaa att gat gtg ccg aat ata ggc cgt ttg aaa gcc acg ctc atc Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile 195 200 205	624
aac gcg ggc att ccg acc gtt ttc ctg aat gcc gcc gac ttg ggc tac Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr 210 215 220	672
acg ggc aaa gag ttg caa gac gac atc aac aac gat gcc gca gct ttg Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu 225 230 235 240	720
gaa aaa ttc gag aaa atc cgc gct tac ggt gcg ctg aaa atg ggt ctg Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu 245 250 255	768
atc agc gac gta tcc gaa gct gcc gcc cgc gcg cac acg ccg aaa gtc Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val 260 265 270	816
gcc ttc gtc gcg ccc gcc gcc gat tac acc gcc tcc agt ggc aaa acc Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr 275 280 285	864
gtg aat gcc gcc gac atc gat ttg ctg gta cgc gcc ctg agc atg ggc Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly	912

aaa ttg cac cac gcg atg atg ggt acc gcc tct gtt gcc att gcg acc 960
 Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr
 305 310 315 320

 gcc gcc gcc gtg ccc ggt acg ctg gtc aac ctt gcc gca ggc ggc gga 1008
 Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Gly Gly
 325 330 335

 acg cgt aaa gaa gtg cgc ttc ggg cat cct tcc ggc aca ttg cgc gtc 1056
 Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
 340 345 350

 ggt gca gcc gcc gaa tgt cag gac gga caa tgg acg gcc acc aaa gcg 1104
 Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala
 355 360 365

 gtt atg agc cgc agc gca cgc gtg atg atg gaa ggt tgg gtc agg gtg 1152
 Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val
 370 375 380

 ccg gaa gat tgt ttt taa 1170
 Pro Glu Asp Cys Phe
 385

<210> 75

<211> 389

<212> PRT

<213> Neisseria meningitidis

<400> 75

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Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu
 20 25 30

Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
 35 40 45

Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
 50 55 60

Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp
 65 70 75 80

Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
 85 90 95

Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
 100 105 110

Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile
 115 120 125

Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala
 130 135 140

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu
 145 150 155 160

Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu
 165 170 175

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Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val
 180 185 190
 Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile
 195 200 205
 Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr
 210 215 220
 Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu
 225 230 235 240
 Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu
 245 250 255
 Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val
 260 265 270
 Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr
 275 280 285
 Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly
 290 295 300
 Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr
 305 310 315 320
 Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Gly Gly
 325 330 335
 Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
 340 345 350
 Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala
 355 360 365
 Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val
 370 375 380
 Pro Glu Asp Cys Phe
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 Met Asn Ser Thr Ala Ser Lys Thr Leu Lys Gly Leu Ser Leu Val Phe
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 ttc gcc tct ggc ttc tgc gcc ctg att tac cag gtc agc tgg cag agg 96
 Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
 20 25 30
 ctt cta ttc agc cac ata ggt atc gat ttg agt tcg att act gtc att 144
 Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile
 35 40 45

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att tct gta ttt atg gtc ggc ttg ggt gta ggt gcg tat ttc ggc gga Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly 50 35 60	192
cgc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile 65 70 75 80	240
gct gaa gta tcc atc ggt ctg ttc ggt ttg gta agc aag ggt ctg att Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Lys Gly Leu Ile 85 90 95	288
tcc ggc ttg ggg cat ctt tta gtt gag gct gat ttg ccc atc atc gct Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala 100 105 110	336
gct gcc aat ttc ctc tta ttg ctg ctt cct acc ttt atg atg ggc gcg Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala 115 120 125	384
acc ttg ccc ttg ctg acc tgt ttt ttt aac cgg aaa ata cat aat gtt Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val 130 135 140	432
ggc gag tct atc ggt acc tta tat ttt ttc aac act ttg ggt gcg gca Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala 145 150 155 160	480
ctc gga tgc ctt gcc gcc gcc gaa ttt ttc tac gtc ttt ttt acc ctc Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu 165 170 175	528
tcc caa acc att gcg ctg aca gcc tgc ctt aac ctt ctg att gct gct Ser Gln Thr Ile Ala Leu Thr Ala Cys Leu Asn Leu Leu Ile Ala Ala 180 185 190	576
tca gta tgc tgc gtt aca gaa agg atg gat atg gtg aac act aaa ccg Ser Val Cys Cys Val Thr Glu Arg Met Asp Met Val Asn Thr Lys Pro 195 200 205	624
aat act agt gtg att aat atg ctt tct ttc ctt acc gga tta ttg agc Asn Thr Ser Val Ile Asn Met Leu Ser Phe Leu Thr Gly Leu Leu Ser 210 215 220	672
ttg ggt ata gaa gtc ttg tgg gta agg atg ttt tgc ttc gca gca cag Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln 225 230 235 240	720
tcc gtg cct cag gca ttt tca ttt att ctt gcc tgt ttt ctg acc ggt Ser Val Pro Gln Ala Phe Ser Phe Ile Leu Ala Cys Phe Leu Thr Gly 245 250 255	768
atc gcc gtc ggc gcg tat ttt ggc aaa cgg att tgc cgc agc cgc ttt Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe 260 265 270	816
gtt gat att ccc ttt atc ggg cag tgc ttc ttg tgg gcg ggt att gcc Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala 275 280 285	864
gat ttt ttg att ttg ggt gct gcg tgg ttg ttg acg ggt ttt tcc ggt Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly 290 295 300	912
ttc gtc cac cac gcc ggt att ttc att acc ctg tct gcc gtc gtc agg Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg	960

305	310	315	320	
ggg ttg att ttc cca'ctt gta cac cat gtg ggt acg gat ggc aac aaa Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys 325 330 335				1008
tcc gga cga cag gtt tcc aat gtt tat ttc gcc aac gtt gcc ggc agt Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser 340 345 350				1056
gca ttg ggt ccg gtc ctt atc ggc ttt gtg ata ctt gat ttg ttg tcc Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Leu Leu Ser 355 360 365				1104
acc caa cag att tac ctg ctc atc tgt ttg att tct gct gct gtc cct Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro 370 375 380				1152
ttg ttt tgt aca ctg ttc caa aaa agt ctc cga ctg aat gca gtg tcg Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser 385 390 395 400				1200
gta gca gtt tcc cta atg ttc ggc atc ctc atg ttc cta ctg ccg gat Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp 405 410 415				1248
tct gtc ttt caa aat att gct ggc cgt ccg gat agg ttg att gaa aac Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn 420 425 430				1296
aaa cac ggc att gtt gcg gtt tac cat aga gat ggt gat aag gtt gtt Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val 435 440 445				1344
tat ggg gcg aat gta tac gac ggc gca tac aat acc gat ata ttc aat Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn 450 455 460				1392
agt gtc aac ggc atc gaa cgt gcc tat ctg cta ccc tcc ctg aag tcc Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser 465 470 475 480				1440
ggc ata cgc cgc att ttc gtc gtt gga ttg agt aca ggt tcg tgg gcg Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala 485 490 495				1488
cgc gtc ttg tct gcc att ccg gaa atg cag tcg atg atc gtt gcg gaa Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu 500 505 510				1536
atc aat ccg gca tac cgt agc ctt atc gcg gac gag ccg caa atc gca Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala 515 520 525				1584
ccg ctt ttg cag gac aaa cgt gtt gaa att gta ttg gat gac ggt agg Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg 530 535 540				1632
aaa tgg ctg cgt cgc cat cct gat gaa aaa ttc gac ctg att ttg atg Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met 545 550 555 560				1680
aat tcg act tgg tac tgg cgt gcc tat tcc act aac ctg ttg agt gcg Asn Ser Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala 565 570 575				1728

gaa ttt tta aaa cag gtg caa agc cac ctt acc ccg gat ggt att gta 1776
 Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val
 580 585 590

 atg ttt aat acc acg cac agc ccg cat gct ttt gct acc gcc gta cac 1824
 Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His
 595 600 605

 agt att ccc tat gca tac cgc tac ggg cat atg gta gtc ggc tcg gca 1872
 Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala
 610 615 620

 acc ccg gta gtt ttc cct aat aaa gaa ctg ctc aag caa cgc ctt tcc 1920
 Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser
 625 630 635 640

 cgg ttg att tgg ccg gaa agc ggc agg cac gta ttt gac agc agc acc 1968
 Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr
 645 650 655

 gtg gat gct gca gca caa aag gtt gtc tct cgt atg ctg att cgg atg 2016
 Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Arg Met
 660 665 670

 acg gaa cct tcg gct ggg gcg gaa gtc att act gac gat aat atg att 2064
 Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile
 675 680 685

 gta gaa tac aaa tac ggc aga ggg att taa 2094
 Val Glu Tyr Lys Tyr Gly Arg Gly Ile
 690 695

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 <213> Neisseria gonorrhoeae

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 Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
 20 25 30

 Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile
 35 40 45

 Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly
 50 55 60

 Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile
 65 70 75 80

 Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Lys Gly Leu Ile
 85 90 95

 Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala
 100 105 110

 Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala
 115 120 125

 Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val
 130 135 140

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Gly	Glu	Ser	Ile	Gly	Thr	Leu	Tyr	Phe	Phe	Asn	Thr	Leu	Gly	Ala	Ala		145	150	155	160
Leu	Gly	Ser	Leu	Ala	Ala	Ala	Glu	Phe	Phe	Tyr	Val	Phe	Phe	Thr	Leu		165		170	175
Ser	Gln	Thr	Ile	Ala	Leu	Thr	Ala	Cys	Leu	Asn	Leu	Leu	Ile	Ala	Ala		180		185	190
Ser	Val	Cys	Cys	Val	Thr	Glu	Arg	Met	Asp	Met	Val	Asn	Thr	Lys	Pro		195		200	205
Asn	Thr	Ser	Val	Ile	Asn	Met	Leu	Ser	Phe	Leu	Thr	Gly	Leu	Leu	Ser		210	215		220
Leu	Gly	Ile	Glu	Val	Leu	Trp	Val	Arg	Met	Phe	Ser	Phe	Ala	Ala	Gln		225	230	235	240
Ser	Val	Pro	Gln	Ala	Phe	Ser	Phe	Ile	Leu	Ala	Cys	Phe	Leu	Thr	Gly		245		250	255
Ile	Ala	Val	Gly	Ala	Tyr	Phe	Gly	Lys	Arg	Ile	Cys	Arg	Ser	Arg	Phe		260		265	270
Val	Asp	Ile	Pro	Phe	Ile	Gly	Gln	Cys	Phe	Leu	Trp	Ala	Gly	Ile	Ala		275		280	285
Asp	Phe	Leu	Ile	Leu	Gly	Ala	Ala	Trp	Leu	Leu	Thr	Gly	Phe	Ser	Gly		290	295		300
Phe	Val	His	His	Ala	Gly	Ile	Phe	Ile	Thr	Leu	Ser	Ala	Val	Val	Arg		305	310	315	320
Gly	Leu	Ile	Phe	Pro	Leu	Val	His	His	Val	Gly	Thr	Asp	Gly	Asn	Lys		325		330	335
Ser	Gly	Arg	Gln	Val	Ser	Asn	Val	Tyr	Phe	Ala	Asn	Val	Ala	Gly	Ser		340		345	350
Ala	Leu	Gly	Pro	Val	Leu	Ile	Gly	Phe	Val	Ile	Leu	Asp	Leu	Leu	Ser		355	360		365
Thr	Gln	Gln	Ile	Tyr	Leu	Leu	Ile	Cys	Leu	Ile	Ser	Ala	Ala	Val	Pro		370	375		380
Leu	Phe	Cys	Thr	Leu	Phe	Gln	Lys	Ser	Leu	Arg	Leu	Asn	Ala	Val	Ser		385	390	395	400
Val	Ala	Val	Ser	Leu	Met	Phe	Gly	Ile	Leu	Met	Phe	Leu	Leu	Pro	Asp		405		410	415
Ser	Val	Phe	Gln	Asn	Ile	Ala	Gly	Arg	Pro	Asp	Arg	Leu	Ile	Glu	Asn		420		425	430
Lys	His	Gly	Ile	Val	Ala	Val	Tyr	His	Arg	Asp	Gly	Asp	Lys	Val	Val		435	440		445
Tyr	Gly	Ala	Asn	Val	Tyr	Asp	Gly	Ala	Tyr	Asn	Thr	Asp	Ile	Phe	Asn		450	455		460
Ser	Val	Asn	Gly	Ile	Glu	Arg	Ala	Tyr	Leu	Leu	Pro	Ser	Leu	Lys	Ser		465	470	475	480
Gly	Ile	Arg	Arg	Ile	Phe	Val	Val	Gly	Leu	Ser	Thr	Gly	Ser	Trp	Ala		485		490	495

093043 03101
T09T80"EE40E860

Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu
500 505 510

Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala
515 520 525

Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg
530 535 540

Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met
545 550 555 560

Asn Ser Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala
565 570 575

Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val
580 585 590

Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His
595 600 605

Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala
610 615 620

Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser
625 630 635 640

Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr
645 650 655

Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Arg Met
660 665 670

Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile
675 680 685

Val Glu Tyr Lys Tyr Gly Arg Gly Ile
690 695

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<211> 39

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32


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<211> 36

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34

<210> 89

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27

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 90

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34

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<223> Description of Artificial Sequence: primer

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33

<210> 97

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<223> Description of Artificial Sequence: primer

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<210> 98

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33

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33

<210> 101

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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30

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<210> 102
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<210> 107
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<223> Description of Artificial Sequence: primer

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<210> 113
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<210> 116
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<400> 118
ggactagtc accatggctg ccaaccaacg ttaccg

36

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34

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29

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33

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27

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<223> Description of Artificial Sequence: primer

09830433-081601

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28

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(21) Numéro de la demande internationale: PCT/FR99/02643 (22) Date de dépôt international: 28 octobre 1999 (28.10.99) (30) Données relatives à la priorité: 98/13693 30 octobre 1998 (30.10.98) FR (71) Déposants (pour tous les Etats désignés sauf US): PASTEUR MERIEUX SERUMS ET VACCINS [FR/FR]; 58, avenue Leclerc, F-69007 Lyon (FR). INSTITUT NATIONAL DE LA SANTÉ ET DE LA RECHERCHE MÉDICALE (INSERM) [FR/FR]; 101, rue de Tolbiac, F-75013 Paris (FR). (72) Inventeurs; et (75) Inventeurs/Déposants (US seulement): AUJAME, Luc [FR/FR]; 477, chemin du Puits, F-69210 Fleurieux-sur-L'Arbresle (FR). BOUCHARDON, Annabelle [FR/FR]; 7, rue Nicolaï, F-69007 Lyon (FR). RENAULD-MONGENIE, Geneviève [FR/FR]; 24, rue des Framboisiers, F-69630 Chaponost (FR). ROKBI, Bachra [FR/FR]; 254, rue Vendôme, F-69003 Lyon (FR). NASSIF, Xavier [FR/FR]; 1, square Charles Laurent, F-75015 Paris (FR). TINSLEY, Colin [FR/FR]; 16, square Jean Thébaud, F-75015 Paris (FR). PERRIN, Agnès [FR/FR]; 33 bis, rue du Docteur Roux, F-75015 Paris (FR).		(74) Mandataires: MONCHENY, Michel etc.; Cabinet Lavoix, 2, place d'Estienne d'Orves, F-75441 Paris Cedex 09 (FR). (81) Etats désignés: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, brevet ARIPO (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), brevet eurasien (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), brevet européen (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), brevet OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Publiée <i>Avec rapport de recherche internationale.</i> (88) Date de publication du rapport de recherche internationale: 17 août 2000 (17.08.00)
(54) Title: <u>NUCLEIC ACIDS AND POLYPEPTIDES SPECIFIC OF THE NEISSERIA GENUS PATHOGENIC STRAINS</u> (54) Titre: ACIDES NUCLEIQUES ET POLYPEPTIDES SPECIFIQUES DES SOUCHES PATHOGENES DU GENRE NEISSERIA (57) Abstract <p>The invention concerns nucleic acids coding for polypeptides specific of the <i>Neisseria</i> genus pathogenic strains, the corresponding polypeptides, and their diagnostic and therapeutic applications.</p> (57) Abrégé <p>Cette invention concerne des acides nucléiques codant pour les polypeptides spécifiques des souches pathogènes du genre <i>Neisseria</i>, les polypeptides correspondants, et leurs applications diagnostiques et thérapeutiques.</p>		

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Nucleic acids and polypeptides specific for pathogenic strains of the *Neisseria* genus.

The present invention relates to nucleic acids encoding polypeptides specific for pathogenic strains of the *Neisseria* genus, in particular which are useful for preventing or treating a *Neisseria meningitidis* infection.

In general, meningitis is either of viral origin or of bacterial origin. The bacteria mainly responsible are: type b *Haemophilus influenzae*, *Neisseria meningitidis* and *Streptococcus pneumoniae*. The *Neisseria meningitidis* species is subdivided into serogroups according to the nature of the capsular polysaccharides. Although about a dozen serogroups exist, 90% of meningitis cases can be attributed to three serogroups: A, B and C.

Effective vaccines based on capsular polysaccharides exist for preventing meningitis caused by *Neisseria meningitidis* serogroups A and C. These polysaccharides, unmodified, are only slightly immunogenic, or not at all, in children under the age of two, and do not induce any immune memory. However, these drawbacks can be overcome by conjugating these polysaccharides to a carrier protein.

On the other hand, the polysaccharide of *Neisseria meningitidis* serogroup B is non-immunogenic, or relatively non-immunogenic in humans, whether or not it is in a conjugated form. Thus, it appears to be highly desirable to seek a vaccine against meningitis caused by *Neisseria meningitidis*, in particular *Neisseria meningitidis* serogroup B, other than a vaccine based on polysaccharide.

To this end, various proteins of the external membrane of *N. meningitidis* have already been proposed, such as the membrane-bound receptor for human transferrin (WO 90/12591 and WO 93/06861).

Neisseria meningitidis is genetically very close to *Neisseria gonorrhoeae* and *Neisseria lactamica*.

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N. gonorrhoeae is especially responsible for infections located in the urogenital tract. It colonizes the genital mucous membrane, crosses the epithelium and then invades the sub-epithelium, where it multiplies and is responsible for a severe inflammatory reaction. On the other hand, *N. lactamica* is considered to be a nonpathogenic species.

Sequences present in *N. gonorrhoeae* and *N. meningitidis*, but absent from *N. lactamica*, have been disclosed in patent application WO 98/02547, but this prior patent application does not locate or identify the coding sequences.

The authors of the present invention have now managed to identify some of these genes by searching, in the meningococcal genome, for the open reading frames specific for pathogenic strains of the *Neisseria* genus, using the following strategy:

Some of the sequences disclosed in patent application WO 98/02547 (referred to, in said prior application, as SEQ ID Nos 66, 67, 69, 70, 72 to 96, 98 and 99) were positioned on the sequence of the genome of the *N. meningitidis* serogroup B strain (ATCC 13090), available from the Pathoseq® bank of Incyte Pharmaceuticals, and also on the sequence of the genome of the *Neisseria meningitidis* strain Z2491 (Sanger Centre). This made it possible to identify, in the *N. meningitidis* genome which has 2.3 mega bases, 19 contigs representing 220 000 base pairs.

The authors of the present invention then analysed, for each of the 19 contigs, the presence of open reading frames (ORFs) containing at least 100 amino acids (and, by definition, bordered by an initiation codon and a stop codon), using the Gene Jockey II sequence processor® program (Biosoft). This analysis made it possible to select approximately 400 candidate ORFs.

The sequences of each of these ORFs were then analysed using the Codon Use® program (Conrad Halling), which takes into account the codon use frequency in

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N. meningitidis. Only the ORFs with sequences having a maximum frequency of use of these codons were selected. At the end of this analysis, 197 candidate ORFs were selected.

5 The ORFs selected using this double analysis were subjected to a homology search through all of the available banks, using the BLASTX® program, from the access to the Pathoseq® bank of Incyte Pharmaceuticals. This homology search made it possible to exclude the
10 ORFs encoding, *a priori*, cytoplasmic or periplasmic proteins, in particular metabolism proteins. The ORFs were also subjected to analysis of possible protein motifs, using the DNA Star Protean® program (Lasergene software).

15 The authors of the present invention then investigated whether the ORFs selected at the end of the previous step (118 in number) were effectively absent from *N. lactamica*, as predicted by the application of the prior art WO 98/02547.

20 To this end, a PCR amplification was carried out. This amplification proved to be ineffective for 78 of the 118 ORFs tested. Only the ORFs for which the amplification in *N. lactamica* was negative (sequences named "lactamica⁻") were selected. In order to verify
25 that these negative results were not "false negatives", the lactamica⁻ sequences selected were subjected to a control by dot blot. At the end of this step, only 23 ORFs were confirmed *N. meningitidis*⁺/*N. lactamica*⁻.

30 Finally, these 23 ORFs were repositioned in their entirety on the *N. meningitidis* ATCC13090 genome. This made it possible to demonstrate that three ORFs previously eliminated on the basis of their putative protein function appeared to be located close to, or were even framed by, some of the 23
35 *N. meningitidis*⁺/*N. lactamica*⁻ ORFs. These three ORFs (SEQ ID Nos 29, 35 and 37) were reintroduced into the study, and it was proven that they were also *N. meningitidis*⁺/*N. lactamica*⁻.

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The authors of the present invention then attempted to discover whether the ORFs identified using the genome of the *N. meningitidis* serogroup B strain ATCC 13090 were also present in the genomes of

5 *N. meningitidis* serogroup A Z2491 (Sanger Centre) and of *N. gonorrhoeae* FA1090 (Advanced Centre of Genome Technology, Oklahoma University). Then, they compared the sequences derived from these various genomes, with multiple alignment (Clustal, Infobiogen). This made it

10 possible to redefine, for some of the ORFs, the most probable position of the initiation codon and translation stop codon. The sequences of the open reading frames derived from the strain ATCC13090 are given in the SEQ ID Nos 1-51 (odd numbers) and the

15 amino acid sequences which are deduced therefrom are given in the SEQ ID Nos 2-52 (even numbers).

A subject of the present invention is, therefore, a nucleic acid in isolated form encoding a polypeptide, or an antigenic fragment thereof,

20 excluding the nucleic acids disclosed in SEQ ID Nos 70, 73, 74, 77, 80, 81, 87, 88, 89, 94, 95 and 98 of application WO 98/02547 (sequences attached to the present description and numbered SEQ ID Nos 70A, 73A, 74A, 77A, 80A, 81A, 87A, 88A, 89A, 94A, 95A and 98A so

25 as to distinguish them from the sequences of the invention); said polypeptide having an amino acid sequence which is identical or homologous to a sequence selected from those of group II; group II consisting of the sequences shown in SEQ ID Nos 2-52 (even numbers)

30 and the sequence SEQ ID No. 53.

Preferably, said nucleic acid can have a nucleotide sequence selected from those of group I, group I consisting of the sequences shown in SEQ ID Nos 1-51 (odd numbers).

35 The term "nucleic acid" includes and means equally ORF, gene, polynucleotide, DNA and RNA. The term "nucleic acid in isolated form" means a nucleic acid separated from the biological environment in which it is found under natural conditions. For example, a

DNA molecule exists under natural conditions when it is integrated into a genome or when it forms part of a library of genes. In that case, it cannot be in isolated form. On the other hand, the same molecule
5 separated from the genome by cloning (for example subsequent to a PCR amplification) should be considered as being in isolated form. Typically, a DNA molecule in isolated form does not contain the coding regions which are contiguous with it in 5' and 3' in the genome from
10 which it is derived. The nucleic acids in isolated form can be integrated into vectors (for example plasmids, or viral or bacterial vectors) without, even so, abandoning their characteristic of being separated from their natural environment.

15 The authors of the present invention have more particularly found that the ORFs which, when they are derived from the strain ATCC 13090, are characterized by the sequences as shown in SEQ ID Nos 19, 27, 39, 45, 47 and 49 are specific for *Neisseria meningitidis*
20 insofar as it has not been possible to demonstrate identical or homologous sequences in the *N. gonorrhoeae* genome. They have also found that the ORF characterized by the strain sequence as shown in SEQ ID No. 39 is specific for *Neisseria meningitidis* serogroup B.

25 A subject of the invention is also a polypeptide in isolated form, or a fragment thereof; said polypeptide having an amino acid sequence identical or homologous to a sequence selected from those of group II.

30 The amino acids framed in the sequence SEQ ID No. 8 correspond to the signal sequence, and the amino acid in bold represents the first amino acid of the mature form. The amino acid sequence of the mature protein form is represented in SEQ ID No. 53.

35 In the context of the present invention, the terms "polypeptide" and "protein" are equivalent and mutually interchangeable. They refer to any amino acid chain, whatever its length and its post-translational

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modifications (for example phosphorylation or glycosylation).

5 The expression "antigenic fragments of the polypeptides specific for pathogenic strains of the *Neisseria* genus" is intended to mean the polypeptides derived from the polypeptides of the invention as defined above, through deletions of portions of said polypeptides without destroying the antigenicity (for example, without notable loss of the antigenic activity) of said polypeptides. The specific antigenicity can be determined using various methods known to those skilled in the art, as explained later.

15 These fragments are preferably at least 12 amino acids long, more preferably at least 20 amino acids long, preferentially 50 amino acids long, more preferably still 75 amino acids long, preferentially 100 amino acids long.

20 These fragments can be used to reveal epitopes which may be masked in the parent polypeptides. They are also advantageous for inducing a T-lymphocyte-dependent protective immune response. The deletions can, in fact, make it possible to eliminate immunodominant regions which are highly variable between various strains.

25 Such fragments can be obtained using standard techniques known to those skilled in the art (for example, Ausubel et al., Current Protocols in Molecular Biology, John Wiley & Sons Inc, 1994), for example by PCR, RT-PCR or treatment with restriction enzymes for the cloned DNA molecules, or by the method of Kunkel et al. (Proc. Natl. Acad. Sci. USA (1985) 82:448).

35 The expression "homologous amino acid sequence" is intended to mean a sequence which differs from one of the sequences of group II by substitution, deletion and/or insertion of one or more amino acids, at positions such that these modifications do not destroy the specific antigenicity of the polypeptide in question.

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Said substitutions are preferably conservative substitutions, i.e. substitutions of amino acids of the same class, such as substitutions of amino acids with uncharged side chains (for instance asparagine, glutamine, serine, threonine and tyrosine), of amino acids with basic side chains (for instance lysine, arginine and histidine), of amino acids with acid side chains (for instance aspartic acid and glutamic acid) or of amino acids with apolar side chains (for instance glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan and cysteine).

Advantageously, a homologous amino acid sequence has at least a 75% degree of homology (i.e. of identity) with one of the sequences of group II; preferably this degree of homology is at least 80%, most preferably at least 90%. The homologous amino acid sequences include, in particular, the sequences which are substantially identical to one of the sequences of group II. The expression "substantially identical sequence" means a sequence which has at least a 90%, advantageously at least a 95%, preferably at least a 97%, and most preferably at least a 99%, degree of homology (i.e. of identity) with one of the sequences of group II. In addition, it may differ from the reference sequence only through mainly conservative substitutions.

The degree of homology (also named degree of identity) is generally determined using a sequence analysis program (for example, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Centre, 1710 University Avenue, Madison, WI 53705). Similar amino acid sequences are aligned so as to obtain the maximum degree of homology (i.e. identity). To this end, it may be necessary to artificially introduce gaps into the sequence. Once optimal alignment has been produced, the degree of homology (i.e. identity) is established by recording all the positions for which the amino acids

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of the two sequences compared are identical, with respect to the total number of positions.

The expression "homologous nucleotide sequences" is intended to mean sequences which differ from the sequences of group I by substitution of one or more nucleotides, or by deletion and/or insertion of one or more codons, at positions such that these sequences (i) still encode polypeptides having the sequences of group II, due to the effect of the degeneracy of the genetic code; or (ii) encode polypeptides having homologous sequences as defined above.

Advantageously, a homologous nucleotide sequence has at least a 60% degree of homology with one of the sequences of group I; preferably this degree of homology is at least 80%, most preferably at least 90%.

Typically, a homologous nucleotide sequence hybridizes specifically to the sequences complementary to the sequences of group I, under stringent conditions. The temperature at which the hybridization assay is carried out constitutes an important factor which influences the stringency. Conventionally, this temperature, termed hybridization temperature (T_h), is selected from 5 to 40°C, preferably from 20 to 25°C, below the temperature at which 50% of the paired strands separate (T_m). In general, it is considered that conditions of high stringency are satisfied when T_h is lower than T_m by 5 to 25°C approximately, for example by 5 to 10°C or, most commonly, by 20 to 25°C approximately. Moderate stringency is established when T_h is lower than T_m by 30 to 40°C.

For sequences comprising more than 30 bases, the temperature T_m is defined by the equation: $T_m = 81.5 + 0.41(\%G+C) + 16.6\log(\text{cation concentration}) - 0.63(\%\text{formamide}) - (600/\text{number of bases})$. Thus, ionic strength has a major impact on the value of T_m . The temperature T_m increases by 16.6°C every time the monovalent cation concentration increases by a factor of 10. The addition of formamide into the hybridization

buffer causes, on the other hand, the value of T_m to decrease. (For a complete reference, see Sambrook et al., Molecular Cloning, A laboratory manual, Cold Spring Harbor Laboratory Press, 1989, pages 9.54-9.62).

5 Conventionally, hybridization experiments are carried out at a temperature of 60 to 68°C, for example at 65°C. At this temperature, stringent hybridization conditions can, for example, be implemented in 6xSSC, advantageously in 2xSSC or 1xSSC, preferably in
10 0.5xSSC, 0.3xSSC or 0.1xSSC (in the absence of formamide). A solution of 1xSSC contains 0.15 M of NaCl and 0.015 M of sodium citrate.

For this reason, in other words, a subject of the invention is a polynucleotide in isolated form,
15 which is capable of hybridizing, under stringent conditions, with a DNA molecule having one of the nucleotide sequences as shown in SEQ ID Nos 1-51 (odd numbers) or the sequences complementary thereto.

A specific class of homologous sequences
20 consists of those encountered naturally by virtue of the extremely common phenomenon of allelic variation. A bacterial species, for example *N. meningitidis* or *N. gonorrhoeae*, consists of a large variety of strains which differ from one another through minor variations,
25 termed allelic variations. Thus, a polypeptide which is present in various strains and which, of course, performs the same biological function in each of them, can have an amino acid sequence which is not identical from one strain to the other. In other words, the
30 sequences derived from the allelic variation are purely sequences equivalent or alternative to those of group II. The class of sequences which are allelic variants of one of the sequences of group II consists of the sequences of the polypeptide as found in a
35 pathogenic species of the *Neisseria* genus (for example, *N. meningitidis* or *N. gonorrhoeae*) other than the *N. meningitidis* strain ATCC 13090. The biological function which is associated with the allelic variant sequences is the same as that which is associated with

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the reference sequence. The differences (substitution, deletion or addition of one or more amino acids) which they exhibit between one another (including the reference sequence) do not modify the biological function of the polypeptide. The term "biological function" is intended to mean the function exercised by the polypeptide in the cells which produce it naturally.

The allelic variation is also expressed in the coding sequences. A polynucleotide, encoding a polypeptide, having a sequence which is an allelic variant of one of the sequences of group I can be easily cloned by amplifying the genomic DNA of the strains of pathogenic species of the *Neisseria* genus, for example by PCR (polymerase chain reaction), using synthetic oligonucleotide primers capable of hybridizing to the 5' and 3' ends of the coding region. The sequences of such primers can easily be established by those skilled in the art using the nucleotide sequences given in SEQ ID Nos 1-51 (odd numbers). The primers generally have from 10 to 40 nucleotides, preferably from 15 to 25 nucleotides.

For this reason, in other words, a subject of the invention is a DNA molecule in isolated form which can be amplified and/or cloned by PCR from the genome of a pathogenic *Neisseria* strain, using a pair of 5' and 3' PCR primers; the sequences of these primers being established using one of the nucleotide sequences as shown in SEQ ID Nos 1-51 (odd numbers). An example is given, for each pair of primers, in Example I.1 hereinafter.

A subject of the present invention is more particularly the allelic variants having the nucleotide sequences SEQ ID Nos 54 to 76 (even numbers) and the products encoded by these nucleotide sequences, having the amino acid sequences SEQ ID Nos 55 to 77 (odd numbers).

The polypeptides of the invention can be fused to other polypeptides, for example by translation of a

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hybrid gene. Vectors for expressing fusion polypeptides are commercially available, such as the vectors pMal-c2 or pMal-p2 from New England Biolabs, in which the protein to which the polypeptides of the invention can be fused is a maltose-binding protein, the glutathione-S-transferase system from Pharmacia or the His-Tag system from Novagen. Such systems are in particular useful for purifying the polypeptides of the invention. The polypeptides of the invention can be fused to polypeptides having adjuvant activity, such as for example the B subunit of cholera toxin or the B subunit of the *E. coli* heat-sensitive toxin.

The nucleic acids of the present invention can be used (i) in a process for producing the polypeptides encoded by said nucleic acids, in a recombinant host system, (ii) for the construction of vaccination vectors, such as poxviruses, intended to be used in methods and compositions for preventing and/or for treating an infection with pathogenic *Neisseria* strains, in particular with *Neisseria meningitidis*, (iii) as a vaccination agent in a naked form or in combination with a vehicle which promotes transfer to the target cells and, (iv) in the construction of attenuated *Neisseria* strains which can overexpress a nucleic acid of the invention, or express it in a non-toxic, mutated form.

The present invention also provides (i) an expression cassette containing a polynucleotide of the invention placed under the control of elements allowing its expression, in particular under the control of a suitable promoter; (ii) an expression vector containing said expression cassette; (iii) a host cell (prokaryotic or eukaryotic) transformed with an expression cassette and/or an expression vector as defined above, and (iv) a method for obtaining a polypeptide encoded by said polynucleotide of the invention, comprising culturing said transformed cell under conditions allowing the expression of the

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polynucleotide of the invention, and recovering the polypeptide from the cell culture.

Among the eukaryotic hosts which can be used, mention may be made in particular of yeast cells (for example *Saccharomyces cerevisiae* or *Pichia Pastoris*), mammalian cells (for example COS1, NIH3T3 or JEG3) arthropod cells (for example *Spodoptera frugiperda* (SF9)) and plant cells. Among the prokaryotic hosts which can be used, mention may be made in particular of *E. coli*.

The choice of the expression cassette depends on the host system chosen, and also on the characteristics desired for the expressed polypeptide. In general, expression cassettes include a promoter which is functional in the host system selected and which can be constitutive or inducible; a ribosome-binding site; an initiation codon (ATG); if necessary, a region encoding a signal peptide; a nucleotide sequence of the invention; a stop codon; and, optionally, a 3' terminal region (translation and/or transcription terminator). The open reading frame (ORF) consisting of the nucleotide sequence of the invention, alone or associated with the region encoding the signal peptide, is placed under the control of the promoter such that translation and transcription take place in the host system. The promoters and regions encoding the signal peptides are known to those skilled in the art. Among them, mention may be made in particular of the arabinose-inducible promoter (araB promoter) of *Salmonella typhimurium*, which is functional in Gram⁻ bacteria such as *E. coli* (US 5,028,530 and Cagnon et al., Protein Engineering (1991) 4(7): 843), the promoter of the T7 bacteriophage gene encoding RNA polymerase (US 4,952,496), and the OspA and RlpB signal peptide (Takase et al., J. Bact. (1987) 169:5692).

The polypeptide expressed can be recovered in a practically purified form from the cell extract or from the supernatant, after centrifuging the recombinant cell culture. The recombinant polypeptide can, in

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particular, be purified using methods of affinity purification with the aid of antibodies, or using any other method known to those skilled in the art, for instance by genetic fusion with a small binding domain.

5 The nucleic acids of the invention can also be used in the field of vaccination, either by using a viral or bacterial host as a vehicle for releasing the DNA, or by administering the nucleic acid of interest in a free form.

10 A subject of the present invention is also (i) a vaccination vector containing a nucleic acid of the invention, placed under the control of elements allowing its expression; (ii) a pharmaceutical composition containing a therapeutically or
15 prophylactically effective amount of said vaccination vector; (iii) a method for inducing an immune response against *Neisseria* in a vertebrate, in particular a mammal, preferably a human, said method comprising the administration to said vertebrate of an immunologically
20 effective amount of said vaccination vector so as to cause an immune response, in particular a protective or therapeutic response to *Neisseria meningitidis*; and (iv) a method for preventing and/or treating an infection with pathogenic *Neisseria* strains, in
25 particular with *Neisseria meningitidis*, which comprises the administration of a prophylactic or therapeutic amount of said vaccination vector of the invention to an individual requiring such a treatment.

 In combination with the polypeptides of the
30 invention, the vaccination vector as defined above can also comprise nucleotide sequences the expression of which allows the immune response to be stimulated, such as the sequences encoding cytokines.

 Said vaccination vector of the invention can be
35 administered via any route which is conventional in the field of vaccination, in particular via the parenteral route (for example subcutaneous, intradermal, intramuscular, intravenous or intraperitoneal route). The dose depends on many parameters which are known to

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those skilled in the art, such as the vector itself, the route of administration, or the weight, age or sex of the animal or of the human to be vaccinated.

5 A subject of the present invention is also (i) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a polynucleotide of the invention; (ii) a method for inducing an immune response against pathogenic *Neisseria* strains, in particular *Neisseria meningitidis*
10 in a vertebrate, by administering to said vertebrate an immunologically effective amount of said polynucleotide so as to cause an immune response, in particular a protective immune response against pathogenic *Neisseria* strains, especially *Neisseria meningitidis*; and (iii) a
15 method for preventing and for treating an infection with pathogenic *Neisseria* strains, in particular with *Neisseria meningitidis*, by administering a therapeutic or prophylactic amount of said polynucleotide to an individual requiring such a treatment.

20 The polynucleotides of the invention (DNA or RNA) can be administered to a vertebrate as they are. When a DNA molecule of the invention is used, it can be in the form of a plasmid incapable of replicating in a vertebrate cell and incapable of integrating the genome
25 of said vertebrate. Said DNA molecule is, typically, placed under the control of a promoter suitable for expression in a vertebrate cell. Said polynucleotide used as vaccine can be formulated according to various methods known to those skilled in the art. Said
30 polynucleotide can, in particular, be used in a naked form, free of any vehicle which promotes transfer to the target cell, such as anionic liposomes, cationic lipids, microparticles, for example gold microparticles, precipitation agents, for example
35 calcium phosphate, or any other agent which facilitates transfection. In this case, the polynucleotide can be simply diluted in a physiologically acceptable solution, such as a sterile solution or a sterile

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buffer solution, in the presence or absence of a vehicle. When it is present, this vehicle can be preferably isotonic, hypotonic or slightly hypertonic, and has a relatively low ionic strength. It can, for example, be a sucrose solution (for example a solution containing 20% of sucrose).

Alternatively, a polynucleotide of the invention can be combined with agents which facilitate transfection. It can be, inter alia, (i) combined with a chemical agent which modifies cell permeability, such as bupivacain (WO 94/16737); (ii) encapsulated in liposomes, optionally in the presence of additional substances which facilitate transfection (WO 93/18759, WO 93/19768, WO 94/25608 and WO 95/2397, WO 93/18759 and WO 93/19768); or (iii) combined with cationic lipids, or silica, gold or tungsten microparticles.

When the polynucleotides of the invention coat microparticles, these particles can be injected via the intradermal or intraepidermal route, using the "gene gun" technique (US 4,945,050, US No. 5,015,580 and WO 94/24263).

The amount of DNA to be used as a vaccine depends, in particular, on the strength of the promoter used in the DNA construct, on the immunogenicity of the product expressed, on the individual to which this DNA is administered, on the method of administration and on the type of formulation. In general, a therapeutically or prophylactically effective amount ranging from approximately 1 µg to approximately 1 mg, preferably from approximately 10 µg to approximately 800 µg, and preferentially from approximately 25 µg to approximately 250 µg, can be administered to human adults.

The polynucleotide of the invention can be administered via any conventional route of administration, such as in particular via the parenteral route. The choice of the route of administration depends, in particular, on the formulation chosen. A polynucleotide formulated in

combination with bupivacain is advantageously administered into muscle. When neutral or anionic liposomes, or a cationic lipid such as DOTMA (N-[1-(2,3-dioleyloxy)propyl]-N,N,N-trimethylammonium chloride) or DC-Chol (3-beta-(N-(N',N'-dimethylaminomethane)carbamoyl)cholesterol) are used, the formulation can advantageously be injected via the intravenous, intramuscular, intradermal or subcutaneous route. A polynucleotide in a naked form can advantageously be administered via the intramuscular, intradermal or subcutaneous route.

The nucleotide sequences of the invention allow the construction of specific nucleotide probes and primers which can be used in diagnosis. Said probes or primers are nucleic acids having sequences identical or homologous to portions of the sequences of group I or to the sequences complementary thereto.

Preferably, said probes contain from approximately 5 to approximately 100, preferably from approximately 10 to approximately 80, nucleotides. They can contain modified bases, the sugar and phosphate residues possibly also being modified or substituted. The probes of the invention can be used in diagnostic tests, to capture or detect polynucleotides specific for pathogenic *Neisseria* strains. Such capture probes can conventionally be immobilized on a solid support directly or indirectly, by covalent bonding or by passive adsorption. A detection probe can be labelled, in particular with a radioactive isotope, an enzyme such as peroxidase or alkaline phosphatase, or enzymes capable of hydrolyzing a chromogenic, fluorogenic or luminescent substrate, or with compounds which are, themselves, chromogenic, fluorogenic or luminescent, nucleotide analogues; or biotin.

A primer generally contains from approximately 10 to approximately 40 nucleotides, and can be used to initiate enzymatic polymerization of the DNA in an amplification process (for example PCR), in an elongation process or in a reverse transcription

method. A primer of the invention can in particular be a primer as described in Example II.1 hereinafter.

A subject of the present invention is also:

(i) a reagent containing a probe of the
5 invention for detecting and/or identifying the presence
of pathogenic *Neisseria* strains in a biological sample;

(ii) a process for detecting and/or for identifying the presence of pathogenic *Neisseria* strains in a biological sample, said method comprising the steps consisting in a) extracting the DNA or RNA from a biological sample and denaturing it; b) exposing said DNA or said RNA to a probe of the invention, under stringent hybridization conditions, so as to detect the hybridization; and

15 (iii) a method for detecting and/or for
identifying pathogenic *Neisseria* strains in a
biological sample, in which the DNA is extracted from a
biological sample and mixed together with at least one
and preferably with two primers of the invention, and
20 is amplified, for example by PCR.

As mentioned above, the polypeptides produced by the expression of the ORF sequences identified can be used as vaccination agents. The specific antigenicity of the polypeptides homologous to the polypeptides having sequences of group II can be evaluated by assaying the cross-reactivity with an antiserum directed against the polypeptides having sequences of group II. A monospecific hyperimmune antiserum can be produced against a purified polypeptide having a sequence of group II or a fusion polypeptide, for example an expression product of the MBP, GST or His-tag systems.

The specific antigenicity can be determined using various methods known to those skilled in the art, in particular the Western blot, dot blot and ELISA techniques, described below.

In the Western blot technique, the protein preparation to be tested is subjected to SDS-PAGE gel electrophoresis. After transfer onto a nitrocellulose

membrane, the material is incubated with a monospecific hyperimmune antiserum obtained after having immunized an animal with the referent material; i.e., in the present case, with a polypeptide having an amino acid sequence of group II. This antiserum is diluted beforehand in a dilution range of approximately 1:50 to 1:5000, preferably of approximately 1:100 to 1:500. The specific antigenicity is revealed when a band corresponding to the product shows reactivity with one of the dilutions above.

In the ELISA assay, a purified protein preparation is preferably used, although a whole cell extract may also be used. Approximately 100 μ l of a preparation at approximately 10 μ g/ml are distributed into the wells of a plate. The plate is incubated for two hours at 37°C, and then overnight at 4°C. The plate is then washed with a phosphate buffered saline solution (PBS) comprising 0.05% of Tween 20. The wells are saturated with 250 μ l of PBS containing 1% of bovine serum albumin (BSA) so as to prevent non-specific antibody binding. After incubation for one hour at 37°C, the plate is washed with the PBS/Tween buffer. The antiserum is serially diluted in PBS/Tween buffer containing 0.5% BSA. 100 μ l of this dilution are added per well. The plate is incubated for 90 minutes at 37°C, washed and evaluated according to standard procedures. For example, when specific antibodies are produced in rabbits, a goat anti-rabbit peroxidase conjugate is added to the wells. The incubation is carried out for 90 minutes at 37°C and the plate is then washed. The reaction is measured by colorimetry (the reaction is positive when the optical density value is 1, if the dilution is at least 1:50, preferably at least 1:500).

In the dot blot assay, a purified protein is preferably used, it being understood that it is also possible to use a whole cell extract. Two-fold serial dilutions of a protein solution at approximately 100 μ g/ml are prepared in a 50 mM Tris-HCl buffer,

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pH: 7.5. 100 µl of each dilution are applied to a nitrocellulose membrane (BioRad apparatus). The buffer is removed by applying suction to the system. The wells are washed by adding 50 mM of Tris-HCl buffer (pH: 7.5) and the membrane is air-dried. The membrane is then saturated in a blocking buffer (50 mM Tris-HCl (pH: 7.5) 0.15 M NaCl, 10 g/l of skimmed milk) and incubated with a dilution of antiserum ranging from approximately 1:50 to 1:5000, preferably to approximately 1:500. The reaction is revealed in accordance with standard procedures. For example, when specific antibodies are produced in rabbits, a goat anti-rabbit peroxidase conjugate is added to the wells. The incubation is carried out for 90 minutes at 37°C. The reaction is developed with the suitable substrate and measured, for example by colorimetry, by the appearance of a coloured spot (a reaction is positive when a coloured spot appears in association with a dilution of at least 1:50, preferably of at least 1:500).

A subject of the present invention is also (i) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a polypeptide of the invention; (ii) a method for inducing an immune response against pathogenic *Neisseria* strains in a vertebrate, by administering to said vertebrate an immunogenically effective amount of a polypeptide of the invention so as to cause an immune response, in particular a protective immune response against pathogenic *Neisseria* strains; and (iii) a method for preventing and/or for treating an infection with pathogenic *Neisseria* strains, by administering a therapeutic or prophylactic amount of a polypeptide of the invention to an individual requiring such a treatment.

The immunogenic compositions of the invention can be administered via any route which is conventional in the field of vaccination, in particular via the parenteral route (for example subcutaneous,

intradermal, intramuscular, intravenous or intra-peritoneal route). The choice of the route of administration depends on a certain number of parameters, such as the adjuvant combined with the
5 polypeptide.

A composition of the invention contains at least one polypeptide as defined above. It can also contain at least one additional antigen of *Neisseria meningitidis* and/or *Neisseria gonorrhoeae*.

10 The polypeptides of the invention can be formulated with liposomes, preferably neutral or anionic liposomes, microspheres, ISCOMS or "virus-like" particles, in order to facilitate the transfer of the polypeptide and/or to increase the immune response.

15 The administration can be carried out with a single dose or with doses repeated, if necessary, at intervals which can be determined by those skilled in the art.

For example, an initial dose can be followed by
20 three booster doses at intervals of one or more weeks or of one or more months. The suitable dose depends on many parameters, including the individual treated (adult or child), the specific vaccination antigen, the route of administration and the frequency of
25 administration, the presence or absence or the type of adjuvant, and the desired effect (for example protection and/or treatment), and can be determined by those skilled in the art. If the route of
administration is parenteral, the dose is
30 preferentially less than 1 mg, preferably approximately 100 µg. The polypeptides and polynucleotides of the invention used as vaccination agents can be used sequentially, in a several-step immunization process. For example, a vertebrate can be initially sensitized
35 with a vaccination vector of the invention, such as a poxvirus, for example via the parenteral route, and can then be stimulated twice with the polypeptide encoded by the vaccination vector.

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FOI b7D b7E b7F b7G b7H b7I b7J b7K b7L b7M b7N b7O b7P b7Q b7R b7S b7T b7U b7V b7W b7X b7Y b7Z

A polypeptide of the invention can also be useful as a diagnostic agent for detecting the presence of anti-*Neisseria meningitidis* and/or anti-*Neisseria gonorrhoeae* antibodies in a biological sample such as a blood sample.

A subject of the present invention is also monospecific antibodies directed against the polypeptides of the invention.

The term "monospecific antibodies" is intended to mean an antibody capable of reacting specifically with a *Neisseria* polypeptide of the invention. Such antibodies can be polyclonal or monoclonal, and can be recombinant antibodies, for example chimeric (for example consisting of a variable region of murine origin associated with a constant region of human origin), humanized and/or single-chain antibodies. Said antibodies can also be in the form of immunoglobulin fragments, for example F(ab)'2 or Fab fragments. The antibodies of the invention can be of any isotype, for example IgA or IgG, the polyclonal antibodies possibly being of a single isotype or possibly containing a mixture of several isotypes.

The antibodies of the invention directed against the polypeptides of the invention can be produced and identified using standard immunological methods, for example Western blot analysis, a dot blot assay, an ELISA assay (Coligan et al., Current Protocols in Immunology (1994) John Wiley & Sons, Inc., New York, NY). Said antibodies can be used in diagnostic processes for detecting the presence of a *Neisseria meningitidis* antigen in a sample such as, in particular, a biological sample (for example a blood sample).

The antibodies of the invention can also be used in affinity chromatography processes for purifying a polypeptide of the invention. Finally, such antibodies can also be used in prophylactic or therapeutic passive immunization methods.

A subject of the present invention is also a diagnostic method for detecting the presence of pathogenic *Neisseria* strains in a biological sample, comprising bringing said biological sample into contact
5 with an antibody or a polypeptide of the invention, such that an immune complex is formed, and detecting said complex which indicates pathogenic *Neisseria* strains in the organism from which the sample originates. Those skilled in the art understand that
10 the immune complex is formed between a component of the sample and the antibody or the polypeptide of the invention, any substance not bound possibly being eliminated prior to the detection of the complex.

Thus, a reagent of polypeptide type can be used
15 for detecting the presence of anti-*Neisseria meningitidis* and/or *Neisseria gonorrhoeae* antibodies in a sample, whereas an antibody of the invention can be used as a reagent for assaying the presence of a *Neisseria meningitidis* and/or *Neisseria gonorrhoeae*
20 polypeptide in a sample.

For use in diagnostic applications, the reagent (for example the antibody or the polypeptide of the invention) can be in the free state or immobilized on a solid support, by direct or indirect means.

25 The direct means include passive adsorption or covalent bonding between the support and the reagent.

The term "indirect means" is intended to mean that a substance which interacts with said reagent is attached to the solid support. For example, if a
30 reagent of polypeptide type is used, an antibody which binds to this polypeptide can be used as an anti-reagent substance, it being understood that this substance binds to an antibody which is not involved in recognizing the antibodies in the biological samples.

35 Among the indirect means which can be used, mention may also be made of the ligand receptor system, a molecule such as a vitamin possibly being grafted onto the reagent of polypeptide type, and the corresponding receptor possibly being immobilized on

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the solid phase. This is illustrated by the biotin-streptavidin system. It is also possible to add a peptide tail to the reagent, by chemical engineering or genetic engineering, and to immobilize the grafted or fused product by passive adsorption or covalent bonding with the peptide tail.

A subject of the present invention is also a process for purifying, from a biological sample, a *Neisseria* polypeptide of the invention, by affinity chromatography with a monospecific antibody of the invention. Said antibody is preferably of isotype IgG.

According to an example of implementation, a biological sample, preferably in a buffer solution, is applied to a chromatographic material, preferably equilibrated with the buffer used to dilute the biological sample, such that the polypeptide of the invention (i.e. the antigen) may adsorb to the material. The unbound components are washed and the antigen is then eluted with a suitable elution buffer, such as a glycine buffer or a buffer containing chaotropic agent, for example guanidine HCl, or a high concentration of salt (for example 3 M MgCl₂). The eluted fractions are recovered and the presence of antigen is detected, for example by measuring the absorbance at 280 nm.

A subject of the present invention is also (i) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a monospecific antibody of the invention; and (ii) a method for preventing and/or for treating an infection with pathogenic *Neisseria* strains, by administering a therapeutic or prophylactic amount of a monospecific antibody of the invention to an individual requiring such a treatment.

To this end, the monospecific antibody of the invention is preferably of isotope IgG, and preferably fixes the complement. Said monospecific antibody according to the invention can be administered alone or in a mixture with at least one other monospecific

antibody, specific for a different *Neisseria meningitidis* and/or *Neisseria gonorrhoeae* polypeptide, according to the invention. The amount of antibody can be determined easily by those skilled in the art. For
5 example, a daily administration of approximately 100 to 1000 mg of antibodies over a week, or three daily doses of approximately 100 to 1000 mg of antibodies over two or three days, may be an effective dose.

The therapeutic or prophylactic effectiveness
10 may be evaluated using standard methods known to those skilled in the art, for example by measuring the induction of an immune response or the induction of protective and/or therapeutic immunity (in newborn rats or mice), through evaluation of the bacterial load in
15 the cerebrospinal fluid. The protection can be determined by comparing the degree of *Neisseria* infection to a control group. Protection is demonstrated when the infection is decreased in comparison with the control group. Such an evaluation
20 can be carried out with the polynucleotides, the vaccination vectors, the polypeptides and also the antibodies according to the invention. The therapeutic or prophylactic effectiveness of a product according to the invention (polynucleotide or polypeptide) can also
25 be evaluated in an assay for bactericidal activity, as described by Danve et al., Vaccine (1993) 11(12):1214 against the meningococcal strain of origin of the polynucleotide or polypeptide used. In the field of meningococcal vaccines, the bactericidal activity assay
30 is, in fact, recognized as being the reference assay based upon which it is possible to make a valid prediction of the vaccination value of a product. Briefly, a product according to the invention is administered to animals such as rabbits in order to
35 produce an antiserum against this product. Then, this antiserum is assayed for its lysis capacity. The bactericidal titre of an antiserum represents the inverse of the dilution of this antiserum for which 50% of the load of meningococci is lysed. The antiserum is

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considered to be bactericidal when the titre is higher than 4, with respect to the meningococcal strain of origin of the polynucleotide or polypeptide used. In that case, the product against which the antiserum was generated is demonstrated to be potentially advantageous from a pharmaceutical point of view.

The following examples illustrate the invention without limiting the scope thereof.

10 Legend of the figure

The attached figure represents the vector pCAMyc-His used as a cloning vector.

15 Details of the strategy for identifying the ORFs:

In order to select the ORF sequences specific for the pathogenic strains of the *Neisseria* genus, a PCR amplification is carried out on the sequences of the 118 ORFs selected after analysis with the Gene Jockey®, Codon Use®, and homology search programs. Only the sequences for which the amplification in *N. lactamica* is negative (sequences named "lactamica") are selected. In order to verify that these negative results are not "false negatives", the lactamica sequences selected are subjected to a dot blot.

A - PCR amplification:

A.1. Extraction of genomic DNAs:

30 The genomic DNAs of all of the *Neisseria* strains used in this study were prepared according to an identical protocol. The *N. meningitidis*, *N. lactamica*, *N. flava*, *N. subflava* and *N. mucosa* strains were cultured on tissues of MHA (Muller Hinton Agar, Difco) medium, and the *N. gonorrhoeae* were cultured on tissues of MHA medium supplemented with 10% of heat-treated horse blood (Biomérieux) and 1% of Isovitalex (Biomérieux). The culturing is carried out under an atmosphere containing 10%

CO₂, overnight at 37°C. Then, the cells are harvested, and washed in PBS phosphate buffer (pH 7.2), and the DNA is extracted according to protocol D of the "Rapid Prep genomic DNA isolation kit for cells and tissue" (Pharmacia Biotech).

The genomic DNAs were then controlled on agarose gel for their completeness and by PCR reaction for their purity.

10 A.2. PCR reaction for screening the ORFs absent in *N. lactamica* 2314:

15 A PCR amplification was carried out on the genomic DNAs of the *N. meningitidis* strain ATCC 13090 and *N. lactamica* strain 2314 (ATCC 23970), according to the following protocol:

20 The PCR reaction was carried out on a 50 µl volume with 10 ng of genomic DNA, 250 µM of each of the dNTPs, 300 nM of each of the primers, 1X Taq DNA polymerase buffer and 2 u of Taq DNA polymerase (Appligène).

The amplification cycles are:

	97°C	45 seconds	25 cycles
25	56°C	1 minute	25 cycles
	72°C	2.30 minutes	25 cycles

30 For each of the ORFs analysed, positive and negative controls for the PCR reaction were carried out. At this stage, only the *N. meningitidis*⁺ and *N. lactamica*- ORFs are selected.

B - Selection of the *N. meningitidis*⁺ *N. lactamica*- ORFs by dot blot on genomic DNA:

35 The absence of a product of PCR amplification of an ORF with genomic DNA of *N. lactamica* 2314 as the matrix does not guarantee the absence of this ORF in the *N. lactamica* 2314 genome. Specifically, a certain variability in the region to which the oligonucleotides

should hybridize may be responsible for the absence of amplified product for a given ORF.

In this context, further verification is carried out by dot blot on genomic DNA, using, as probe, the products of genomic amplification on the *N. meningitidis* strain corresponding to each of the reading frames identified. The dot blot filters contain genomic DNA of the following strains: 2 *N. lactamica* strains 8064 and 2314, one *N. flava* strain ATCC 30008, one *N. mucosa* strain ATCC 9297, 3 *N. meningitidis* serogroup B strains ATCC13090, M982 and B16B6, one *N. meningitidis* serogroup A strain Z2491, one *N. meningitidis* serogroup C strain (strain Z4182) and 2 *N. gonorrhoeae* strains MS11 and FA1090. This dot blot analysis makes it possible to validate the absence of the ORF in *N. lactamica* 2314 and 8064, and it is also an indication of the degree of variability of an ORF within the *Neisseria* strains.

The dot blot technique used is as follows. Approximately 50 ng of genomic DNA, denatured for 5 min at 100°C, of the various *Neisseria* strains are loaded, with suction, onto a Hybond N+ nitrocellulose membrane (Amersham) placed between the jaws of a dot blot apparatus (BioRad). Then, the DNA is fixed on the membranes for 5 min with UV radiation at 315 nm.

The membranes are incubated in a prehybridization buffer (containing denatured salmon sperm DNA). They are then hybridized with a probe corresponding to the product of amplification of the ORF of interest, labelled according to a cold labelling protocol, such as the "DIG DNA labelling and detection kit" system (Boehringer Mannheim).

The ORF which does not hybridize to the genomic DNA of *N. lactamica* 2314 and 8064 is definitively selected as a potential vaccination candidate.

Example I: Cloning

1. PCR amplification

5 Each of the ORFs was amplified by PCR using the genomic DNA of *N. meningitidis* serogroup B (strain ATCC 13090), according to standard protocol.

10 Two oligonucleotides, primers on the N-terminal side and on the C-terminal side were defined for each of the ORF sequences of the invention.

15 The primer on the N-terminal side comprises an enzyme restriction site for cloning, a CCACC Kozak sequence for translation initiation (M. Kozak, J. Mol. Biol. 196: 947-950), the ATG of the potential ORF and approximately 17 bases specific for the 5' portion of the ORF.

20 The primer on the C-terminal side was defined such that the ORF cloned is in fusion, in its 3' portion, with a repeat of 8 histidines and a stop codon which are present in the vector behind the multiple cloning site, hence the insertion of an "A" base in order to keep the correct reading frame after cloning and the disappearance of the stop codon of the ORF. The primer on the C-terminal side thus comprises an enzyme
25 restriction site for cloning, an "A" base, and then approximately 20 bases specific for the 3' portion of the gene starting from the codon preceding the stop codon.

30 After searching for restriction sites which are absent in each of the ORFs, with the aid of the DNASTAR MapDraw subprogram (Lasergene Software), the XbaI restriction site in 5' and BglII restriction site in 3' are used for the ORF SEQ ID No. 19. For the ORF SEQ ID No. 41, the SpeI site in 5' and the BglII site in 3'
35 are used. The XbaI restriction site in 5' and BamHI restriction site in 3' are used to clone the remaining ORFs.

 The PCR mixture comprises, for a final volume of 100 µl, 10-50 ng of genomic DNA, the N-terminal and

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C-terminal primers each at 200 nM, the dNTPs each at 250 μ M, the 1X PCR buffer (composition of the 10X PCR buffer: 200 mM Tris-HCl (pH 8.8), 20 mM MgSO₄, 100 mM KCl, 100 mM (NH₄)₂SO₄, 1% TritonX-100 and 1 mg/ml of nuclease-free bovine serum albumin) and 2.5 U of polymerase.

The amplification is carried out as follows:

Step	Temperature (°C)	Time (min.)	Number of cycles
Denaturation	97	0.45	25
Hybridization	cf. table	1	25
Elongation	72	1/kb DNA	25

10

The primers used and the PCR conditions given in the table below, in which "N. g allelic variant" means that an allelic variant is present in *Neisseria gonorrhoeae* and "N. m A allelic variant" means that an allelic variant is present in *Neisseria meningitidis* serogroup A.

15

ORF No. (internal ref.)	SEQ ID No.	5' Primer	3' Primer	Polymerase	Hybridization T°
22	1-2 N.g allelic variant: 54, 55	GCT CTA GAC CAC CAT GTC TGA AGA AAA ATT GAA AAT GAG (SEQ ID n° 78)	CGG GAT CCA GAA ATG GCT GGA TTC GCT ATC AG (SEQ ID n° 79)	Tfu (Appligene)	56°C
41	3-4	GCT CTA GAC CAC CAT GAA ACA CTT ACT CAT CG (SEQ ID n° 80)	CGG GAT CCA ATA CGT AGG ACT TGG GTC (SEQ ID n° 81)	Tfu (Appligene)	43°C
42-43	5-6 N.g allelic variant: 56, 57	GCT CTA GAC CAC CAT GAA AAA ATC (CCT TTT CGT TC (SEQ ID n° 82)	CGG GAT CCA TTG CGG ATA AAC ATA TTC CGC C (SEQ ID n° 83)	Tfu (Appligene)	56°C
47	7-8 N.g allelic variant: 58, 59	GCT CTA GAC CAC CAT GCG AAC GAC CCC AAC CTT C (SEQ ID n° 84)	CGG GAT CCA GAA CCG GTA GCC TAC GCC GAC (SEQ ID n° 85)	Tfu (Appligene)	56°C
55	9-10 N.g allelic variant: 60, 61	GCT CTA GAC CAC CAT GAA CAC ACG CAT CAT CGT TTC (SEQ ID n° 86)	CGG GAT CCA GCA ACG GCC TGC CGC TTT AAG (SEQ ID n° 87)	Pfu Turbo (Stratagene)	56°C
68	11-12	GCT CTA GAC CAC CAT GCT GAC GTT TAT CGG ACT G (SEQ ID n° 88)	CGG GAT CCA CGG CAG AGG CAC GAT TCC (SEQ ID n° 89)	Tfu (Appligene)	56°C

ORF No. (internal ref.)	SEQ ID No.	5' Primer	3' Primer	Polymerase	Hybridization T°
71	13-14	GCT CTA GAC CAC CAT GGG CAT CCA TCT CGA CTT C (SEQ ID n° 90)	CGG GAT CCA CAA AAG TTC CAG AAA AIC TAA CTC (SEQ ID n° 91)	Tfu (Appligene)	56°C
72	15-16 N.mA. allelic variant: 62, 63	GCT CTA GAC CAC CAT GAA TAG ACC CAA GCA ACC (SEQ ID n° 92)	CUG GAT CCA TGC CGC TTG GGG GAG GC (SEQ ID n° 93)	Pfu Turbo (Stratagene)	56°C
73	17-18 N.g allelic variant: 64, 65	GCT CTA GAC CAC CAT GAT GAA TGT CGA GGC AGA G (SEQ ID n° 94)	CGG GAT CCA CAG TTT GCC CGA CAT AC (SEQ ID n° 95)	Pfu Turbo (Stratagene)	56°C
74	19-20	GCT CTA GAC CAC CAT GAA ATT TTT TCC TGC TCC (SEQ ID n° 96)	GAA GAT CTA GAA ACT GTA ATT CAA GTT GAA G (SEQ ID n° 97)	Pfu Turbo (Stratagene)	56°C
98	21-22	GCT CTA GAC CAC CAT GAT TGA ATT TGT CCG AGC (SEQ ID n° 98)	CGG GAT CCA ACC CIG CGA CGA GTT GCG (SEQ ID n° 99)	Pfu Turbo (Stratagene)	56°C
116	23-24 N.g.allelic variant: 66, 67	GCT CTA GAC CAC CAT GCA ATA CAG CAC ACT GGC (SEQ ID n° 100)	CGG GAT CCA GTC CTT TTT CGC ACC TTG AAG (SEQ ID n° 101)	Pfu Turbo (Stratagene)	56°C
122	25-26	GCT CTA GAC CAC CAT GGA GCA GTC GGG CAA ATT C (SEQ ID n° 102)	CGG GAT CCA AGC TGT TTG GCG ATT TCG GTG (SEQ ID n° 103)	Pfu Turbo (Stratagene)	56°C

ORF No. (internal ref.)	SEQ ID No.	5' Primer	3' Primer	Polymerase	Hybridization T°
125	27-28	GCT CTA GAC CAC CAT GCA AAA CCG CGG GGG AAA G C (SEQ ID n° 104)	CGG GAT CCA GTG CCT GCG CAG CTT GGA ATC (SEQ ID n° 105)	Pfu Turbo (Stratagene)	56°C
128	29-30 N.mA. allelic variant: 68, 69	GCT CTA GAC CAC CAT GAC ATT GCT CAA TCT AAT GAT AAT G (SEQ ID n° 106)	CGG GAT CCA TTC CGC AAA TAC CTG TIT CCA ACC (SEQ ID n° 107)	Tfu (Appligene)	56°C
152	31-32 N.g allelic variant: 70, 71	GCT CTA GAC CAC CAT GAA ACA ATC CGC CCG (SEQ ID n° 108)	CGG GAT CCA TAC TTG GGC GCA ACA TGA C (SEQ ID n° 109)	Pfu Turbo (Stratagene)	56°C
153	33-34	GCT CTA GAC CAC CAT GAA TGT TTA CGG TTT CTT (SEQ ID n° 110)	CGG GAT CCA TTT TTT AGA CGT ATT TTT AGT CG (SEQ ID n° 111)	Tfu (Appligene)	56°C
155	35-36	GCT CTA GAC CAC CAT GAT GAG TCA ACA CTC TCG C (SEQ ID n° 112)	CGG GAT CCA TCC AGT TTT TGC TCG AAG GC (SEQ ID n° 113)	Tfu (Appligene)	56°C
156	37-38	GCT CTA GAC CAC CAT GCC TTC GAG CAA AAA CTG G (SEQ ID n° 114)	CGG GAT CCA TCG TTC TTC AAT CTC CAC AAA CG (SEQ ID n° 115)	Tfu (Appligene)	56°C
157	39-40	GCT CTA GAC CAC CAT GCA CC TGG AAA G (SEQ ID n° 116)	CGG GAT CCA TTC AAT TCG CTT CAA CAA TG (SEQ ID n° 117)	Tfu (Appligene)	56°C

ORF No. (internal ref.)	SEQ ID No.	5' Primer	3' Primer	Polymerase	Hybridization T°
158	41-42 N.mA. allelic variant: 72, 73	GGA CTA GTC CAC CAT GGC TGC CAA CCA ACG TTA CCG (SEQ ID n° 118)	GAA GAT CTA AGC CGC GTT CCG TTC CAA AAA ATC (SEQ ID n° 119)	Tfu (Appligene)	56°C
159	43-44 N.mA. allelic variant: 74, 75	GCT CTA GAC CAC CAT GCC GCA AAT TAA AAT TCC C (SEQ ID n° 120)	CGG GAT CCA AAA ACA A TC TTC CGG CAC CC (SEQ ID n° 121)	Tfu (Appligene)	56°C
161	45-46	GCT CTA GAC CAC CAT GCG CAC GGC GTT TTG TTG (SEQ ID n° 122)	CGG GAT CCA TTG GGC AAC GAC GAA GGC AC (SEQ ID n° 123)	Tfu (Appligene)	56°C
163-1	47-48	GCT CTA GAC CAC CAT GAG AAT AGA GAT CAC ACC (SEQ ID n° 124)	CGG GAT CCA TGG CTC AAT CCT TTC TGC (SEQ ID n° 125)	Pfu Turbo (Stratagene)	56°C
163-2	49-50	GCT CTA GAC CAC CAT GAT TCA CGT TTC GGC AGT G (SEQ ID n° 126)	CGG GAT CCA ACC TGC TTC ATG GGT (GAT TC (SEQ ID n° 127)	Tfu (Appligene)	56°C
167-168	51-52 N.gallelic variant: 76, 77	GCT CTA GAC CAC CAT GAA TTC GAC CGC AAG TAA AAC (SEQ ID n° 128)	CGG GAT CCA AAT CCG TCT GCC GTA TTT G (SEQ ID n° 129)	Tfu (Appligene)	56°C

2- Cloning, transformation and selection of recombinants

The cloning vector used is the 6.357 kb vector pCA/Myc-His or pM1070 (cf. figure), derived from the plasmid pCDNA 3.1 (Invitrogen). pCA/Myc-His comprises, in particular, the CMV iel promoter (bases 249-902), intron A of the CMV iel gene (Chapman et al., 1991 Nucleic Acids Research, 19, 3979-3986), a multiple cloning site (bases 1792-1852) with the PmlI, EcoRV, NotI, XbaI, BamHI, KpnI and HindIII sites, a sequence encoding a polyhistidine and a stop codon (bases 1908-1928), a bgh 3' termination sequence (bases 1853-2197) and the ampicillin resistance gene for selecting the recombinant clones in *E. coli*.

After purification (GeneClean Bio101 kit), the PCR amplification products are digested for 2 hours at 37°C with the appropriate enzymes (XbaI-BamHI, XbaI-BglII or SpeI-BglII), in a final reaction volume of 20 µl. The digestion products are then ligated with the vector pCA/Myc-His, digested beforehand with XbaI and BamHI, according to the "Rapid DNA Ligation Kit" protocol (Boehringer Mannheim). 15 µl of the ligation is used to transform 100 µl of competent *E. coli* XLI-blue cells (Novagen). The cells are incubated for 30 minutes in ice, 30 seconds at 42°C and 2 minutes in ice. Then, 500 µl of LB medium without antibiotics are added, and the mixture is incubated for 1 hour at 37°C. Next, 50 and 550 µl of the culture are plated out on plates containing LB medium plus ampicillin (50 µg/ml final concentration), and incubated overnight at 37°C.

The following day, 36 colonies are placed in culture in 2 ml of LB plus ampicillin (50 µg/ml) and incubated overnight at 37°C.

The following day, the plasmid DNA is extracted according to the Qiagen mini-prep protocol (Qiagen) and the recombinants are identified by enzymatic restriction followed by agarose gel electrophoresis. The cloning junctions are then verified by sequencing.

Example II: Evaluation of the protective activity of the ORFs of the invention

5 A. Preparation of the DNA intended for the immunization experiments:

An isolated colony of a recombinant clone is used to inoculate a preculture in LB medium + ampicillin, and 5 ml of this preculture represents the
10 inoculum of a 2.5 litre culture in LB medium + ampicillin. The purification protocol for preparing the plasmid DNA is that described in the EndoFree Giga Kit (Qiagen). The purified DNA is eluted from the
15 purification column with a 10 mM Tris-HCl, 1 mM EDTA buffer, pH 8, and stored at -20°C. Before injection, the purified recombinant plasmid is diluted to 100 µg/ml with water (of injectable preparation quality) and the NaCl concentration is brought to 150 mM.

20 B. Production of a specific polyclonal serum:

B.1. Hyperimmunization in an animal model:

25 The animal model used is the mouse or the rabbit. The route of administration of the injected DNA is the intramuscular or intradermal route. The recombinant plasmids to be injected are optionally applied to beads if they are injected into animals
30 using a gene gun apparatus (BioRad). The immunization protocol follows a scheme comprising two injections, 3 weeks apart.

35 B.2. Analysis of the bactericidal activity of the antibodies induced:

Ten days after the final injection, the animals are bled and the sera are analysed using the bactericidal activity assay according to the protocol of Danve et al., Vaccine (1993) 11 (12):1214. Briefly,

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a. Preparation of transformants:

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b. Production of the protein:

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2. Protein purification

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supernatant is filtered through a 0.45 μ m membrane. The supernatant is loaded onto an IMAC column (12 ml of resin) which has been prepared by immobilizing Ni⁺⁺ cations according to the manufacturer's recommendations (Pharmacia). The column is washed with 10 column volumes of 20 mM Tris-HCl (pH 8.0), 0.5 M NaCl, 60 mM imidazole. The recombinant protein is eluted with six volumes of 20 mM Tris-HCl (pH: 7.9), 0.5 M NaCl, 500 mM imidazole, 0.1% Zwittergent 3-14.

The elution profile is controlled by measuring the absorbence of the fractions at an optical density of 280 nm. An aliquot fraction is analysed on an SDS-PAGE gel and stained with Coomassie blue (Phast System - Pharmacia), and the fractions corresponding to the protein peak are then pooled and concentrated. In order to eliminate the elution buffer, the fraction is passed over a G24 Sephadex column (Pharmacia) and equilibrated in PBS buffer (pH: 7.4). The protein solution is sterilized by filtration through a 0.45 μ m membrane, and the protein concentration is determined using the BCA micromethod (Pierce). The protein solution is stored at -70°C.

Example IV: Production of monospecific polyclonal antibodies

1. Rabbit hyperimmune antiserum

100 μ g (in total) of the polypeptide purified in Example III, in the presence of complete Freund's adjuvant in a total volume of approximately 2 ml, are injected into New Zealand rabbits, both subcutaneously and intravenously. 21 and 42 days after the initial injection, the booster doses, which are identical to the initial doses, are administered in the same way, with the exception that incomplete Freund's adjuvant is used. 15 days after the final injection, the animal's serum is recovered, decomplemented and filtered through a 0.45 μ m membrane.

2. Mouse hyperimmune ascites fluid

10-50 µg of the purified fusion polypeptide obtained in Example II, in the presence of complete Freund's adjuvant, in a volume of approximately 200 µl, are injected subcutaneously into 10 mice. 7 and 14 days after the initial injection, booster doses, which are identical to the initial doses, are administered in the same way, with the exception that incomplete Freund's adjuvant is used. 21 and 28 days after the initial injection, the mice receive 50 µg of the antigen alone, intraperitoneally. On the 21st day, the mice are also injected intraperitoneally with 180/TG CM26684 sarcoma cells (Lennette & Schmidt, Diagnostic procedures for viral, rickettsial, and chlamydial infections, (1979) 5th Ed. Washington DC, American Public Health Association). The ascites fluids are harvested 10 to 13 days after the first injection.

Example V: Purification of the polypeptides of the invention by immunoaffinity

1. Purification of specific IgG

An immune serum as prepared in Example IV is applied to a Fast Flow Sepharose 4 protein A column (Pharmacia) equilibrated with 100 mM Tris-HCl (pH: 8.0). The resin is washed by applying 10 column volumes of 100 mM Tris-HCl and 10 volumes of 10 mM Tris-HCl (pH: 8.0) to the column. The IgGs are eluted with a 0.1 M glycine buffer (pH: 3.0) and are collected by 5 ml fraction, to which 0.25 ml of 1 M Tris-HCl (pH: 8.0) are added. The optical density of the eluate is measured at 280 nm and the fractions containing the IgGs are pooled and, if necessary, stored at -70°C.

2. Column preparation

A suitable amount of CNBr-activated Sepharose 4B gel (1 g of dried gel providing approximately 3.5 ml of hydrated gel, and the capacity of the gel ranging from 5 to 10 mg of coupled IgG per ml of gel)

manufactured by Pharmacia (17-0430-01) is suspended in 1 mM HCl buffer and washed, using a Buchner funnel, by adding small amounts of 1 mM HCl buffer. The total volume of the buffer is 200 ml per gram of gel.

5 The purified IgGs are dialysed for four hours at $20 \pm 5^\circ\text{C}$ against 5 volumes of 500 mM PBS buffer (pH: 7.5). Then, they are diluted in 500 mM of PBS (pH: 7.5) for a final concentration of 3 mg/ml.

10 The IgGs are incubated with the gel overnight at $5 \pm 3^\circ\text{C}$, with stirring. The gel is packed into a chromatography column and washed with 2 column volumes of 500 mM phosphate buffer (pH: 7.5) and then one volume of 50 mM NaCl sodium buffer (pH: 7.5). The gel is then transferred to a tube, then incubated with 15 100 mM of ethanolamine (pH: 7.5) for 4 hours at room temperature with stirring, and then washed twice with two column volumes of PBS. The gel is then stored in PBS merthiolate at 1/10 000. The amount of IgG coupled to the gel is determined by measuring the optical 20 density at 280 nm of the IgG solution and of the direct eluate.

3. Adsorption and elution of the antigen

25 A solution of antigen in 50 mM Tris-HCl (pH: 8.0), 2 mM EDTA, for example the supernatant obtained in Example III.2 after treatment with Benzonase, centrifugation and filtration through a 0.45 μm membrane, is applied to a column equilibrated with 50 mM Tris-HCl (pH: 8.0), 2 mM EDTA, at a flow 30 rate of approximately 10 ml/hour. Then, the column is washed with 20 volumes of 50 mM Tris-HCl (pH: 8.0), 2 mM EDTA. Alternatively, batch adsorption can be carried out, in which the mixture is left overnight at $5 \pm 3^\circ\text{C}$, with stirring.

35 The gel is washed with 2 to 6 volumes of 10 mM PBS buffer (pH: 6.8). The antigen is eluted with a 100 mM glycine buffer (pH: 2.5). The eluate is collected in 3 ml fractions, to which 150 μl of 1 mM PBS buffer (pH: 8.0) are added. The optical density is

measured at 280 nm for each fraction; those containing the antigen are recovered and stored at -20°C.

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Fragments of the genome of *N. meningitidis* Z2491
described in patent application WO 98/02547

(2) INFORMATION FOR SEQ ID NO: 70A:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15

(iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70A:

GATCAGACCC ATTTTCAGCG CACCGTAAGC GCGGATTTTC TCGAATTTTT CCAAAGCTGC 60
GGCATCGTTG TTGATGTCGT CTGCAACTC TTTGCCCGTG TAGCCCAAGT CGGCGGCATT 120
CAGGAAAACG GTCGGAATGC CCGCGTTGAT GAGCGTGGCT TTCAAACGGC CTATATTCGG 180
CACATCAATT TCATCGACCA AATTGCCGCT TGGGAACATA CTGCCTTCGC CGTCGGCTGG 240
ATC 243

20

(2) INFORMATION FOR SEQ ID NO: 73A:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 120 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73A:

5

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60

ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

(2) INFORMATION FOR SEQ ID NO: 74A:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

20

(iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74A:

CGGTCAGAAA CAGGCAAGGT AATGAAAATG CCTGAGGCAC GGACTGTGCT GCGAACGAAA 60

ACTCCTTACC GAAGTCTTCT ATACCCAGGC TCAATAGCCG CTCAAGGAGA GAGCTATCAT 120

25

(2) INFORMATION FOR SEQ ID NO: 77A

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 base pairs

30

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35

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F09T80*E40E860

(iii) HYPOTHETICAL: NO

(iv) ANTISENS: NO

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77A:

```
CGGAGCATAA AATCGTTATT AAAGATAATG GTATAGGAAC GAGCTTCGAT GAAATCAATG      60
ATTTTATTTT GAGAATCGGT CGGAACAGAA GGGAAGAAAA ACAAGCCTCC CCGTGCGGAA      120
GAATTCCAAC GGGTAAAAAA GGCCTTGCTA AATTGGCATT ATTCGGGCTT GGCAACAAAA      180
TTGAAATTTC TACTATCCAG GGAAACGAAA GGGTTACTTT TACTTTGGAT TATGCAGAGA      240
TTCGAAGAAG CAAGGGTATT TATCAACCG      269
```

(2) INFORMATION FOR SEQ ID NO: 80A:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

20

(iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80A:

```
CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTTT GGCTTGACAG TTTGGAAATA      60
TTGTGTATCG GGGGGGGGTA TTGCTGACG TAAAAAACTA TAAACGCCGC GCAAAATATG      120
GCTGACTATA TTATTGACTT TGATTTTGTG CTGCGCGGTG ATGGATAAAA TCGCCAGCGA      180
TAAAGAATTT GCGAGAACCT GATGCCG      207
```

25

(2) INFORMATION FOR SEQ ID NO: 81A:

098043-08404

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 base pairs

(B) TYPE: nucleotide

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iii) HYPOTHETICAL: NO

(iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81A:

15

CGGCAACGAT TTGAGCTATC GCGGTTACGA CATTCTGGAT TTGGCACAAA AATGCGAGTT 60

TGAAGAAGTC GCCCACCTGC TGATTCACGG CCATCTGCCC AACAAATTCG AGCTGGCCGC 120

TTATAAAACC AAGCTCAAAT CCATGCGCGG CCTGCCTATC CGTGTGATTA AAGTTTGGGA 180

AAGCCTGCCT GCACATACCC ATCCGATGGA CGTAATGCGT ACCG 224

(2) INFORMATION FOR SEQ ID NO: 87A:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs

(B) TYPE: nucleotide

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

30 (iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87A:

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FOI 80-0040360


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AATTTCCACC TATGCCCTAC GCAGCGATTA TCCGTGGTTT ACCCAAAGGG TGATTATGGC      60
AAAAGCGCGG GGTGAGCGA CCGCCTTTTG TTGCCGGCGT TCAAACGGGT TTTGATAGGA      120
AATGCAGGCA CGAAGCCTCG GCTGATTGTG ATGCACCTGA TGGGTTCGCA CAGTGATTTT      180
TGCACACGTT TGGATAAGGA TCGCGGCGG TTTCAGTATC AACTGAAAA AATATCCTGC      240
TATGTTTCCA TCAATCGCGC AAACCGATAA ATT                                     273

```

(2) INFORMATION FOR SEQ ID NO: 88A:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

15

- (iv) ANTISENS: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88A:

```

AATTCTTCCG CACGGGGAAG CTGTTTTTC TTCCCTCTG TTCCGACCGA TTCTCAAATA      60
AAAATCATTG ATTTCAICGA AGTTCATTC TATACCATTA TCTTTAATAA CGATTTTATG      120
CTCCGTTTGA TCGAATAACC TAACTTCCAC TTCCGTAGCA CATGCATCGT AGGCATTCGC      180
TATCAACTCG GCAATCGCAG GAACAGTGTG CGAATACAAT CTTTACACCC AAATGTTTGA      240
TTACGGTTGG CTCGAAACTC AATTTCAATT                                     270

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20

(2) INFORMATION FOR SEQ ID NO: 89A:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single

25

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (iii) HYPOTHETICAL: NO

(iv) ANTISENS: NO

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89A:

AATTATGAAC ACACGCATCA TCGTTTCGGC TCGTTTCGTT GCGTTGGCAT TAGCAGGTTG 50
CGGCTCAATC AATAATGTAA CCGTTTCCGA CCAGAAACTT CAGGAACGTG CCGCGTTTGC 100
CTTGGGCGTC ACCAATGCCG TAAAAATCAG CAACCGCAGC AATGAAGGCA TACGCATCAA 150
CTTTACCGCA ACTGTGGGTA AGCGCGTGAC CAATGCTATG TTACCACTGT AATCAGCACA 200
ATCGGCGGTA CCACTTCCGA TGCAATT 267

(2) INFORMATION FOR SEQ ID NO: 94A:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

25 (iv) ANTISENS: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94A:

```

AATTTGTTGG GCAGATGGCC GTGAATCAGC A3GTGGGCGA CTTCTTCAAA CTCGCATTTT      60
TOTGCCAAAT CCAGAATGTC GTAACCGCGA TACGTCAAAT CGTTGCCGGT ACGCAACGGT      120
ACACAAAGCG GTATTACCGG CCGCAACGCC AGAAAGCGCA ACGGATTTTT AGGTTTGAGG      180
GTCGGGGTTT GAGTAGTTTC AGTCAIGGTA TTTCTCCTTT GTGTTTTTAT GGGTTTCGGG      240
TTTTCAGACG ACCGATGCGG ATTTGTTGAA AGGCAGTCTG AAAGCGGTAA ATCATTTTGT      300
AAACAATT .                               308

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(2) INFORMATION FOR SEQ ID NO: 95A:

- 5 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTISENS: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95A:

```

AATTCGGAGG AGCAGTACCG CCAAGCGTTG CTCGCCTATT CCGGCGGTGA TAAACAGAC      60
GAGGGTATCC GCCTGATGCA ACAGAGCGAT TACGGCAACT TGTCCTACCA CATCCGTAAT      120
AAAAACATGC TTTTCATTTT TTCGGCAAGC AATGACGCAC AAGCTCAGCC CAACACAAC      180
GACCCTATTG CCATTTTATG AAAAAGACGC TCAAAAAGGC ATTATCACAG TTGCAGGCGT      240
AGACCGCAGT GGAGAAAAGT TCAATGGCTC CAACCATTTG GGAATT                      286

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20

(2) INFORMATION FOR SEQ ID NO: 98A:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs

(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTISENS: NO

10

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093043 041601

CLAIMS

1. Nucleic acid in isolated form, encoding a polypeptide specific for the pathogenic strains of the *Neisseria* genus, or antigenic fragment thereof, excluding the sequences SEQ ID Nos 70A, 73A, 74A, 77A, 80A, 81A, 87A, 88A, 89A, 94A, 95A and 98A, the amino acid sequence of said specific polypeptide being identical or homologous to a sequence selected from the sequences of group II, group II consisting of the sequences SEQ ID No. 2 to SEQ ID No. 52 (even numbers) and the sequence SEQ ID No. 53.
2. Nucleic acid according to Claim 1, the nucleotide sequence of which is identical or homologous to a sequence selected from the sequences of group I, group I consisting of the sequences SEQ ID No. 1 to SEQ ID No. 51 (odd numbers).
3. Nucleic acid according to Claim 1, encoding a polypeptide specific for the pathogenic strains of the *Neisseria* genus, or antigenic fragment thereof, the amino acid sequence of said specific polypeptide being selected from the sequences SEQ ID Nos 55 to 77 (odd numbers).
4. Nucleic acid according to Claim 3, having a nucleotide sequence selected from the sequences SEQ ID Nos 54 to 76 (even numbers).
5. Polypeptide specific for the pathogenic strains of the *Neisseria* genus, and antigenic fragments thereof, the amino acid sequence of said specific polypeptide being identical or homologous to a sequence selected from the sequences of group II, consisting of the sequences SEQ ID No. 2 to SEQ ID No. 52 (even numbers) and the sequence SEQ ID No. 53.

6. Polypeptide according to Claim 5, specific for the pathogenic strains of the *Neisseria* genus, and antigenic fragments thereof, the amino acid sequence of said specific polypeptide being selected from the sequences SEQ ID Nos 55 to 77 (even numbers).

7. Expression vector comprising an expression cassette in which a nucleotide sequence as defined in one of Claims 1 to 4 is placed under conditions allowing its expression in a host cell.

8. Host cell transformed with the expression vector according to Claim 7.

9. Pharmaceutical composition comprising:

a) a nucleic acid according to one of Claims 1 to 4, in naked form or in combination with at least one agent facilitating transfection;

b) or a vaccination vector comprising a nucleotide sequence as defined in one of Claims 1 to 4, such as in particular a virus or a bacterium;

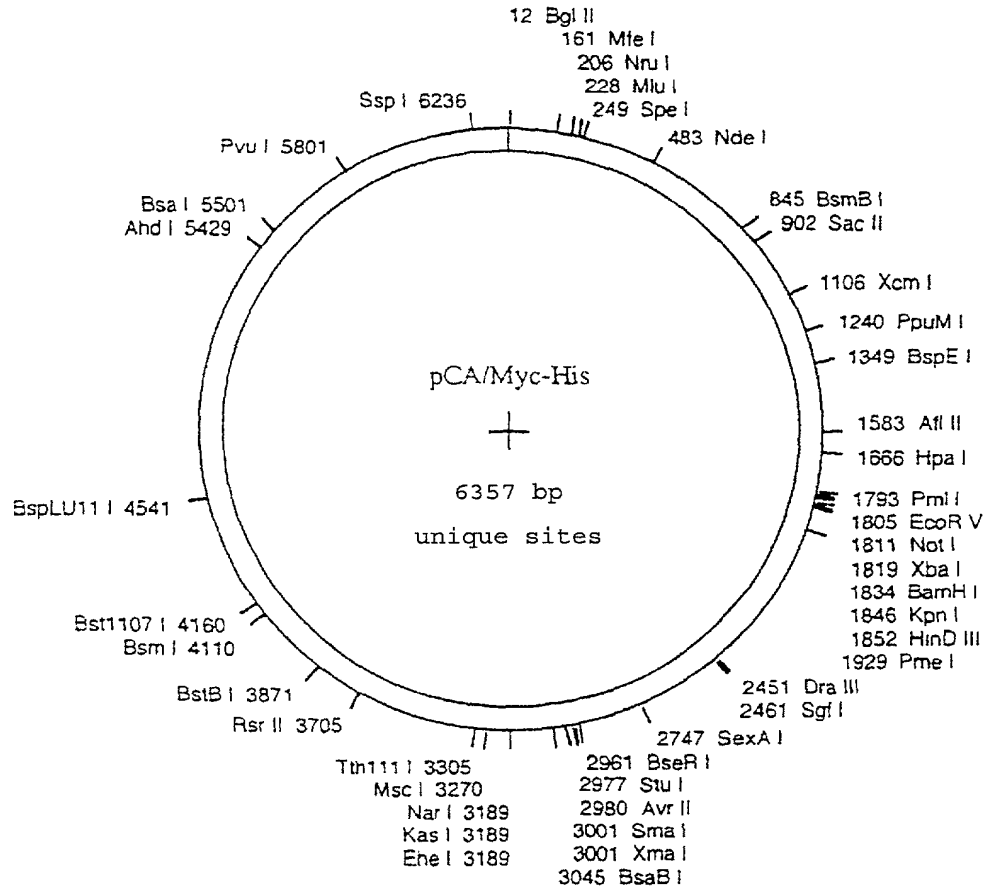
c) or a polypeptide according to either of Claims 5 and 6;

optionally in combination with a pharmaceutically acceptable vehicle.

10. Monospecific antibody directed against a polypeptide according to either of Claims 5 and 6.

11. Use of a nucleic acid according to one of Claims 1 to 4, or of a polypeptide specific for pathogenic *Neisseria* strains or of antigenic fragments thereof, according to either of Claims 5 and 6, for manufacturing a pharmaceutical composition intended for vaccination against *Neisseria*.

1/1



09/830433-001

DECLARATION FOR USA PATENT APPLICATION

(including Design and National Stage PCT)

Attorney's Docket ID: _____

As a below named inventor, I hereby declare that:

My residence, mailing address and citizenship are as stated below adjacent to my name. I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought

on the invention entitled: Nucleic acids and polypeptides specific of the Neisseria genus
the specification of which: pathogenic strains

_____ is attached hereto.

(or)

☒ was filed on 26.04.2001 as U.S. Application No. or PCT International Application No. 09/830433

and (if applicable) was amended on _____

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment specifically referred to above. I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR 1.56.

I hereby claim foreign priority benefits under 35 U.S.C. 119(a)-(d) or 365(b) of any foreign application(s) for patent or inventor's certificate, or 365(a) of any PCT International application which designated at least one country other than the United States of America, listed below and have also identified below, where priority is not claimed, any foreign application for patent or inventor's certificate, or any PCT International application, having a filing date before that of the application on which priority is claimed. (____ ADDITIONAL APPLICATIONS IDENTIFIED ON ATTACHED SHEET)

Prior Foreign Application No.	Country	Day/Month/Year Filed	Priority Not Claimed
<u>FR 98 13693</u>	<u>FRANCE</u>	<u>30.10.98</u>	<u>_____</u>

I hereby claim the benefit under 35 U.S.C. 120 of any U.S. application(s), or 365(c) of any PCT application designating the U.S., listed below; and insofar as the subject matter of each claim of this application is not disclosed in the prior U.S. or PCT application in the manner provided by the first paragraph of 35 U.S.C. 112, I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR 1.56 which became available between the filing date of the prior application and the national or PCT filing date of this application. (____ ADDITIONAL APPLICATIONS IDENTIFIED ON ATTACHED SHEET.)

U.S. or PCT Parent Application No.	Parent Filing Date (Day/Month/Year)	Parent Patent No. (if applicable)
<u>PCTFR99/02643</u>	<u>28.10.1999</u>	<u>_____</u>

As a named inventor, I hereby appoint the registered practitioners of LARSON & TAYLOR, PLC associated with Customer Number 000881 to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith. Direct all correspondence to that Customer Number.

Customer No 00881Direct all telephone calls to _____
at TEL (703) 739-4900 (Fax: 703-739-9577) e-mail: _____

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. 1000 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

SOLE OR FIRST INVENTOR		Citizenship
Given Name (first and Middle [if any])	<u>Luc</u>	<u>French</u>
Full Mailing Address	<u>477, Chemin du Puits - 69210 FLEURIEUX SUR L'ABRESLE - FRANCE</u>	Family Name or Surname <u>AUJAME</u>
Residence - City, State/Country (if different from PO address)	<u>same as above</u>	
SIGN AND DATE HERE Inventor's Signature <u>[Signature]</u>		Date <u>9.7.2001</u>
SECOND JOINT INVENTOR (if any)		Citizenship
Given Name (first and Middle [if any])	<u>Annabelle</u>	<u>French</u>
Full Mailing Address	<u>7, rue Nicolai - 69007 LYON - FRANCE</u>	Family Name or Surname <u>BOUCHARDON</u>
Residence - City, State/Country (if different from PO address)	<u>same as above</u>	
SIGN AND DATE HERE Inventor's Signature <u>[Signature]</u>		Date <u>31.7.2001</u>
THIRD JOINT INVENTOR (if any)		Citizenship
Given Name (first and Middle [if any])	<u>Geneviève</u>	<u>French</u>
Full Mailing Address	<u>24, rue des Framboisiers - 69630 CHAPONOST - FRANCE</u>	Family Name or Surname <u>RENAULD-MONGENIE</u>
Residence - City, State/Country (if different from PO address)	<u>same as above</u>	
SIGN AND DATE HERE Inventor's Signature <u>[Signature]</u>		Date <u>10.07.2001</u>
FOURTH JOINT INVENTOR (if any)		Citizenship
Given Name (first and Middle [if any])	<u>Bachra</u>	<u>French</u>
Full Mailing Address	<u>254, rue Vendôme - 69003 LYON - FRANCE</u>	Family Name or Surname <u>ROKBI</u>
Residence - City, State/Country (if different from PO address)	<u>same as above</u>	
SIGN AND DATE HERE Inventor's Signature <u>[Signature]</u>		Date <u>11.07.2001</u>

LARSON & TAYLOR, PLC • 1199 North Fairfax Street • Suite 900 • Alexandria Virginia 22314

11/98

DECLARATION FOR USA PATENT APPLICATION

(including Design and National Stage PCT)

ADDITIONAL INFORMATION SHEET (use as required)

I hereby claim the benefit under 35 U.S.C. 119(e) of any United States PROVISIONAL application(s) listed below.

U.S. Provisional Application No.

Parent Filing Date (Day/Month/Year)

Additional Prior Foreign Application(s)

Prior Foreign Application No.

Country

Day/Month/Year Filed

Priority Not Claimed

Additional 35 U.S.C. § 120 application(s):

U.S. or PCT Parent Application No.

Parent Filing Date (Day/Month/Year)

Parent Patent No. (if applicable)

Additional Joint Inventor(s):

FIFTH JOINT INVENTOR (if any)

Citizenship

French

Family Name
or Surname

NASSIF

Given Name (first
and Middle [if any]) Xavier

Full Mailing Address 1, Square Charles Laurent- 75015 PARIS - FRANCE

FRX

Residence - City, State/Country
(if different from PO address) same as above

SIGN AND
DATE HERE Inventor's Signature

Date

20 June 2001

SIXTH JOINT INVENTOR (if any)

Citizenship

British

Family Name
or Surname

TINSLEY

Given Name (first
and Middle [if any]) Colin

Full Mailing Address 16, Square Jean Thébaud - 75015 PARIS - FRANCE

FRX

Residence - City, State/Country
(if different from PO address) same as above

SIGN AND
DATE HERE Inventor's Signature

Date

7 June 2001

SEVENTH JOINT INVENTOR (if any)

Citizenship

French

Family Name
or Surname

PERRIN

Given Name (first
and Middle [if any]) Agnès

Full Mailing Address 33 bis, rue du Docteur Roux - 75015 PARIS - FRANCE

FRX

Residence - City, State/Country
(if different from PO address) same as above

SIGN AND
DATE HERE Inventor's Signature

Date

19 June 2001

EIGHTH JOINT INVENTOR (if any)

Citizenship

Family Name
or Surname

Given Name (first
and Middle [if any])

Full Mailing
Address

Residence - City, State/Country
(if different from PO address)

SIGN AND
DATE HERE Inventor's Signature

Date

09/830433

531 Rec'd PCT 26 APR 2001

WO 00/26375

- 1 -

PCT/FR99/02643

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Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu Gly 485 490 495		
Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn Ile 500 505 510		
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09630433-084601

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Met Ala Leu Ala Val Ala Thr Thr Leu Ser Ala Cys Leu Gly Gly Gly	
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ggc ggc act tct ggc ccc gac ttc aat gca ggc ggc acc ggt atc ggc	144
Gly Gly Thr Ser Ala Pro Asp Phe Asn Ala Gly Gly Thr Gly Ile Gly	
35 40 45	
agc aac agc aga gca aca aca gcg aaa tca gca gca gta tct tac gcc	192
Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala	
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Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly	
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cgg gat gac gtt gcg gtt aca gac agg gat gcc aaa atc aat gcc ccc	288
Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro	
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ccc ccg aat ctg cat acc gga gac ttt aca aac cca aat gac gca tac	336
Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn Pro Asn Asp Ala Tyr	
100 105 110	
aag aat ttg atc aac ctc aaa cct gca att gaa gca ggc tat aca gga	384
Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly	
115 120 125	
cgc ggc gta gag gta ggt atc gtc gat aca ggc gaa tcc gtc ggc agc	432
Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser	
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ata tcc ttt ccc gaa ctg tat ggc aga aaa gaa cac ggc tat aac gaa	480
Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu	
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Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp	
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Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp Asp Glu Ala Val Ile	
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gag act gaa gca aag ccg acg gat atc cgc cac gta aaa gaa atc gga	624
Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly	
195 200 205	
cac atc gat gtg gtc tcc cat att att ggc ggc cgt tcc gtc gac ggc	672
His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly	
210 215 220	

009180"EE40E360

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Thr	His	Asp	Gly	Thr	Lys	Asn	Glu	Ile	Met	Ser	Ala	Ala	Ile	Arg	Asn	
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Ala	Trp	Val	Lys	Leu	Gly	Glu	Arg	Gly	Val	Arg	Ile	Val	Asn	Asn	Ser	
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Phe	Gly	Thr	Thr	Ser	Arg	Ala	Gly	Thr	Ala	Asp	His	Phe	Gln	Ile	Ala	
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Asn	Ser	Glu	Glu	Gln	Tyr	Arg	Gln	Ala	Leu	Leu	Ala	Tyr	Ser	Gly	Gly	
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Asp	Lys	Thr	Asp	Glu	Gly	Ile	Arg	Leu	Met	Gln	Gln	Ser	Asp	Tyr	Gly	
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Asn	Leu	Ser	Tyr	His	Ile	Arg	Asn	Lys	Asn	Met	Leu	Phe	Ile	Phe	Ser	
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Ala	Ser	Asn	Asp	Ala	Gln	Ala	Gln	Pro	Asn	Thr	Leu	Thr	Leu	Leu	Pro	
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Phe	Tyr	Glu	Lys	Asp	Ala	Gln	Lys	Gly	Ile	Ile	Thr	Val	Ala	Gly	Val	
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Asp	Arg	Ser	Gly	Glu	Lys	Phe	Asn	Gly	Ser	Asn	His	Cys	Gly	Ile	Thr	
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gcc	atg	tgg	tgc	cta	tcg	gca	ccc	tat	gaa	gca	agc	gtc	cgt	ttc	acc	1200
Ala	Met	Trp	Cys	Leu	Ser	Ala	Pro	Tyr	Glu	Ala	Ser	Val	Arg	Phe	Thr	
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cgt	aca	aac	cgg	att	caa	att	gcc	gga	aca	tcc	ttt	tcc	gca	ccc	atc	1248
Arg	Thr	Asn	Pro	Ile	Gln	Ile	Ala	Gly	Thr	Ser	Phe	Ser	Ala	Pro	Ile	
				405					410					415		
gta	acc	ggc	acg	gcg	gct	ctg	ctg	ctg	cag	aaa	tac	ccg	tgg	atg	agc	1296
Val	Thr	Gly	Thr	Ala	Ala	Leu	Leu	Leu	Gln	Lys	Tyr	Pro	Trp	Met	Ser	
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Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe Gly Asp Phe Thr Ala	
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gat acg aaa ggt aca tcc gat att gcc tac tcc ttc cgt aac gac att	1488
Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser Phe Arg Asn Asp Ile	
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Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly Ser Gln Leu Gln Leu	
500 505 510	
cac ggc aac aac acc tat acg ggc aaa acc att atc gaa ggc ggt tcg	1584
His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile Ile Glu Gly Gly Ser	
515 520 525	
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Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met Arg Val Glu Thr Lys	
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Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg Ser Gly Ala Asn Glu	
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acc gtg cac atc aaa ggc gat ctg cag ctg ggc ggc gaa ggt acg ctg	1776
Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly Gly Glu Gly Thr Leu	
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Tyr Thr Arg Leu Gly Lys Leu Lys Val Asp Gly Thr Ala Met Thr	
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aac cgt acc gga caa cgt gtt ccc ttc ctg agt gcc gcc aaa atc ggc	1920
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Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr Asp Gly Gly Leu Leu	
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660 665 670	
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gcg gca cat tcc gcg ccc gcc ggt ctg aaa cac gcc gta gaa cag ggc	2112
Ala Ala His Ser Ala Pro Ala Gly Leu Lys His Ala Val Glu Gln Gly	
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tcc gca aca ccc gag acg gtt gaa act gcg gcc gcc gac cgc aca gat Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala Ala Asp Arg Thr Asp 725 730 735	2208
atg ccg ggc atc cgc tac ggc gca act ttc cgc gca gcg gca gcc Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe Arg Ala Ala Ala Ala 740 745 750	2256
gta cag cat gcg aat gcc gcc gac ggt gta cgc atc ttc aac agt ctc Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu 755 760 765	2304
gcc gct acc gtc tat gcc gac agt acc gcc gcc cat gcc gat atg cag Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln 770 775 780	2352
gga cgc cgg ctg aaa gcc gta tgc gac ggg ttg gac cac aac gct acg Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Ala Thr 785 790 795 800	2400
ggc ctg cgc gtc atc gcg caa acc caa cag gac ggt gga acg tgg gaa Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu 805 810 815	2448
cag gcc ggt gtt gaa gcc aaa atg cgc gcc agt acc caa acc gtc gcc Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly 820 825 830	2496
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cgc agc acc ggt gcg gac gaa cat gcg gaa gcc agc gtc aac gcc acg Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr 900 905 910	2736
ctg atg cag ctg gcc gca ctg gcc ggt gtc aac gtt ccg ttt gcc gca Leu Met Gln Leu Gly Ala Leu Gly Val Asn Val Pro Phe Ala Ala 915 920 925	2784
acg gga gat ttg acg gtc gaa gcc ggt ctg cgc tac gac ctg ctc aaa Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys 930 935 940	2832

cag gat gca ttc gcc gaa aaa ggc agt gct ttg ggc tgg agc ggc aac 2880
Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn
945 950 955 960

agc ctc act gaa ggc aca ctg gtc gga ctc gcg ggt ctg aag ctg tgg 2928
Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser
965 970 975

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Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu
980 985 990

cgc gac ctg aac gga cgc gac tac acg gta acg ggc ggc ttt acc ggc 3024
Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly
995 1000 1005

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Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr
1010 1015 1020

cgc ctg gtt gcc ggt ctg ggc gcg gat gtc gaa ttc ggc aac ggc tgg 3120
Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp
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Ser Asn Ser Arg Ala Thr Thr Ala Lys Ser Ala Ala Val Ser Tyr Ala
50 55 60

Gly Ile Lys Asn Glu Met Cys Lys Asp Arg Ser Met Leu Cys Ala Gly
65 70 75 80

Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala Lys Ile Asn Ala Pro
85 90 95

Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn Pro Asn Asp Ala Tyr
100 105 110

Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu Ala Gly Tyr Thr Gly
 115 120 125
 Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly Glu Ser Val Gly Ser
 130 135 140
 Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu His Gly Tyr Asn Glu
 145 150 155 160
 Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys Glu Ala Pro Glu Asp
 165 170 175
 Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp Asp Glu Ala Val Ile
 180 185 190
 Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His Val Lys Glu Ile Gly
 195 200 205
 His Ile Asp Val Val Ser His Ile Ile Gly Gly Arg Ser Val Asp Gly
 210 215 220
 Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr Leu His Ile Met Asn
 225 230 235 240
 Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser Ala Ala Ile Arg Asn
 245 250 255
 Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg Ile Val Asn Asn Ser
 260 265 270
 Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp His Phe Gln Ile Ala
 275 280 285
 Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu Ala Tyr Ser Gly Gly
 290 295 300
 Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln Gln Ser Asp Tyr Gly
 305 310 315 320
 Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met Leu Phe Ile Phe Ser
 325 330 335
 Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr Leu Thr Leu Leu Pro
 340 345 350
 Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile Thr Val Ala Gly Val
 355 360 365
 Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn His Cys Gly Ile Thr
 370 375 380
 Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala Ser Val Arg Phe Thr
 385 390 395 400
 Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser Phe Ser Ala Pro Ile
 405 410 415
 Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys Tyr Pro Trp Met Ser
 420 425 430

09030433 081501

Asn	Asp	Asn	Leu	Arg	Thr	Thr	Leu	Leu	Thr	Thr	Ala	Gln	Asp	Ile	Gly	435	440	445
Ala	Val	Gly	Val	Asp	Ser	Lys	Phe	Gly	Trp	Gly	Leu	Leu	Asp	Ala	Gly	450	455	460
Lys	Ala	Met	Asn	Gly	Pro	Ala	Ser	Phe	Pro	Phe	Gly	Asp	Phe	Thr	Ala	465	470	475
Asp	Thr	Lys	Gly	Thr	Ser	Asp	Ile	Ala	Tyr	Ser	Phe	Arg	Asn	Asp	Ile	485	490	495
Ser	Gly	Thr	Gly	Gly	Leu	Ile	Lys	Lys	Gly	Gly	Ser	Gln	Leu	Gln	Leu	500	505	510
His	Gly	Asn	Asn	Thr	Tyr	Thr	Gly	Lys	Thr	Ile	Ile	Glu	Gly	Gly	Ser	515	520	525
Leu	Val	Leu	Tyr	Gly	Asn	Asn	Lys	Ser	Asp	Met	Arg	Val	Glu	Thr	Lys	530	535	540
Gly	Ala	Leu	Ile	Tyr	Asn	Gly	Ala	Ala	Ser	Gly	Gly	Ser	Leu	Asn	Ser	545	550	555
Asp	Gly	Ile	Val	Tyr	Leu	Ala	Asp	Thr	Asp	Arg	Ser	Gly	Ala	Asn	Glu	565	570	575
Thr	Val	His	Ile	Lys	Gly	Asp	Leu	Gln	Leu	Gly	Gly	Glu	Gly	Thr	Leu	580	585	590
Tyr	Thr	Arg	Leu	Gly	Lys	Leu	Leu	Lys	Val	Asp	Gly	Thr	Ala	Met	Thr	595	600	605
Gly	Gly	Lys	Leu	Tyr	Met	Ser	Ala	Arg	Gly	Lys	Gly	Ala	Gly	Tyr	Leu	610	615	620
Asn	Arg	Thr	Gly	Gln	Arg	Val	Pro	Phe	Leu	Ser	Ala	Ala	Lys	Ile	Gly	625	630	635
Arg	Asp	Tyr	Ser	Phe	Phe	Thr	Asn	Ile	Glu	Thr	Asp	Gly	Gly	Leu	Leu	645	650	655
Ala	Ser	Leu	Asp	Ser	Val	Glu	Lys	Thr	Ala	Gly	Ser	Glu	Gly	Asp	Thr	660	665	670
Leu	Ser	Tyr	Tyr	Val	Arg	Arg	Gly	Asn	Ala	Ala	Arg	Thr	Ala	Ser	Ala	675	680	685
Ala	Ala	His	Ser	Ala	Pro	Ala	Gly	Leu	Lys	His	Ala	Val	Glu	Gln	Gly	690	695	700
Gly	Ser	Asn	Leu	Glu	Asn	Leu	Met	Val	Glu	Leu	Asp	Ala	Ser	Glu	Ser	705	710	715
Ser	Ala	Thr	Pro	Glu	Thr	Val	Glu	Thr	Ala	Ala	Ala	Asp	Arg	Thr	Asp	725	730	735
Met	Pro	Gly	Ile	Arg	Pro	Tyr	Gly	Ala	Thr	Phe	Arg	Ala	Ala	Ala	Ala	740	745	750

09830433-081604

Val Gln His Ala Asn Ala Ala Asp Gly Val Arg Ile Phe Asn Ser Leu
755 760 765

Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala His Ala Asp Met Gln
770 775 780

Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu Asp His Asn Ala Thr
785 790 795 800

Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp Gly Gly Thr Trp Glu
805 810 815

Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser Thr Gln Thr Val Gly
820 825 830

Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala Ala Ala Thr Leu Gly
835 840 845

Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala Asn Ala Lys Thr Asp
850 855 860

Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp Ala Gly Asp Ile Gly
865 870 875 880

Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr Lys Asn Ser Ile Ser
885 890 895

Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly Ser Val Asn Gly Thr
900 905 910

Leu Met Gln Leu Gly Ala Leu Gly Gly Val Asn Val Pro Phe Ala Ala
915 920 925

Thr Gly Asp Leu Thr Val Glu Gly Gly Leu Arg Tyr Asp Leu Leu Lys
930 935 940

Gln Asp Ala Phe Ala Glu Lys Gly Ser Ala Leu Gly Trp Ser Gly Asn
945 950 955 960

Ser Leu Thr Glu Gly Thr Leu Val Gly Leu Ala Gly Leu Lys Leu Ser
965 970 975

Gln Pro Leu Ser Asp Lys Ala Val Leu Phe Ala Thr Ala Gly Val Glu
980 985 990

Arg Asp Leu Asn Gly Arg Asp Tyr Thr Val Thr Gly Gly Phe Thr Gly
995 1000 1005

Ala Thr Ala Ala Thr Gly Lys Thr Gly Ala Arg Asn Met Pro His Thr
1010 1015 1020

Arg Leu Val Ala Gly Leu Gly Ala Asp Val Glu Phe Gly Asn Gly Trp
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Asn Gly Leu Ala Arg Tyr Ser Tyr Ala Gly Ser Lys Gln Tyr Gly Asn
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His Ser Gly Arg Val Gly Val Gly Tyr Arg Phe
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<213> Neisseria meningitidis

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gca ggt tgc ggc tca atc aat aat gta acc gtt tcc gac cag aaa ctt 96
Ala Gly Cys Gly Ser Ile Asn Asn Val Thr Val Ser Asp Gln Lys Leu
          20           25          30

cag gaa cgt gcc gcg ttt gcc ttg ggc gtc agc caa aat gcc gta aaa 144
Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys
          35           40          45

atc agc aac cgc agc aat gaa agc ata cgc atc aac ttt acc gca act 192
Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr
          50           55          60

gtg ggt aag cgc gtg agc caa tgc tat gtt acc agt gta atc agc aca 240
Val Gly Lys Arg Val Ser Gln Cys Tyr Val Thr Ser Val Ile Ser Thr
          65           70          75          80

atc ggc gtt acc act tcc gat gca att tgt ttg gga ggc gga acg cac 288
Ile Gly Val Thr Thr Ser Asp Ala Ile Cys Leu Gly Gly Gly Thr His
          85           90          95

aaa ggc aaa agt caa tgc aat gct ttg ctt aaa gcg gca ggc cgt tgc 336
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          20           25          30

Gln Glu Arg Ala Ala Phe Ala Leu Gly Val Ser Gln Asn Ala Val Lys
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Ile Ser Asn Arg Ser Asn Glu Ser Ile Arg Ile Asn Phe Thr Ala Thr
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Ile Gly Val Thr Thr Ser Asp Ala Ile Cys Leu Gly Gly Gly Thr His		
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Lys Gly Lys Ser Gln Cys Asn Ala Leu Leu Lys Ala Ala Gly Arg Cys		
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1 5 10 15	
ctg ctg acg gaa aaa gtg tgg ccc atc atc gca tta atc ttg gtg ccg	96
Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro	
20 25 30	
ctg ttt ggg gcg ttg ctg gcg ggg ttt gat gta tcc caa tta aaa gaa	144
Leu Phe Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu	
35 40 45	
ttt tat tgg ggc ggc acc aaa tgg gtg atg cag att gtg att atg ttt	192
Phe Tyr Ser Gly Gly Thr Lys Ser Val Met Gln Ile Val Ile Met Phe	
50 55 60	
atg ttt tcc att ttg ttt ttt gga atc atg aac gat gtg ggg ctg ttc	240
Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe	
65 70 75 80	
cgt ccg atg ata ggc ggt ttg att aag ctg act cgg ggt aat atc gtg	288
Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val	
85 90 95	
gca gtg agt gtg ggg acg gtc ttg gtg tgg gtg ggc cag ttg gac	336
Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp	
100 105 110	
ggg gcg ggt gcg acg acg ttt tta ttg gtc gtc ccc gcc ctt ttg ccg	384
Gly Ala Gly Ala Thr Thr Phe Leu Leu Val Val Pro Ala Leu Leu Pro	
115 120 125	
ctt tac aag cgt ctg cat atg aat oct tac ctg ctg ttt ttg ctg ctg	432
Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu	
130 135 140	
act tcc agt gcg gga ttg att aac ctt ctg ccg tgg ggc ggg ccg acc	480

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Thr	Ser	Ser	Ala	Gly	Leu	Ile	Asn	Leu	Leu	Pro	Trp	Gly	Gly	Pro	Thr		
145					150					155					160		
ggg	cgg	gtt	gca	agc	gtg	ttg	ggc	gca	gat	gtg	ggc	gaa	ttg	tat	aaa	528	
Gly	Arg	Val	Ala	Ser	Val	Leu	Gly	Ala	Asp	Val	Gly	Glu	Leu	Tyr	Lys		
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cct	ttg	ttg	acg	gtg	caa	att	atc	ggc	gtg	gtg	ttt	atc	ctt	gcg	ctg	576	
Pro	Leu	Leu	Thr	Val	Gln	Ile	Ile	Gly	Val	Val	Phe	Ile	Leu	Ala	Leu		
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tcc	ctg	ctt	ttg	ggc	gtg	cgt	gaa	aaa	agg	cgg	att	gtc	cgg	gag	ttg	624	
Ser	Leu	Leu	Leu	Gly	Val	Arg	Glu	Lys	Arg	Arg	Ile	Val	Arg	Glu	Leu		
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ggc	gcg	ttg	ccc	gcc	gtg	ggc	gat	ttg	ata	aag	cgc	gtg	ctt	ttg	tcg	672	
Gly	Ala	Leu	Pro	Ala	Val	Ala	Asp	Leu	Ile	Lys	Pro	Val	Pro	Leu	Ser		
	210					215					220						
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Glu	Glu	Glu	Gln	Lys	Leu	Ala	Arg	Pro	Lys	Leu	Phe	Trp	Trp	Asn	Val		
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ctg	ctg	ttt	ttg	ggc	ggc	atg	agg	ctg	ctt	ttt	tcg	ggc	atc	ttc	cgc	768	
Leu	Leu	Phe	Leu	Ala	Ala	Met	Ser	Leu	Phe	Phe	Ser	Gly	Ile	Phe	Pro		
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cgc	ggc	tat	gta	ttt	atg	ctg	gct	gca	acg	ggc	ggc	ttg	ctt	ttg	aat	816	
Pro	Gly	Tyr	Val	Phe	Met	Leu	Ala	Ala	Thr	Ala	Ala	Leu	Leu	Leu	Asn		
			260					265					270				
tac	cgc	agc	cgc	cag	gaa	cag	atg	gag	cgg	att	tat	gcc	cac	gcc	ggc	864	
Tyr	Arg	Ser	Pro	Gln	Glu	Gln	Met	Glu	Arg	Ile	Tyr	Ala	His	Ala	Gly		
		275					280					285					
ggc	ggc	gtg	atg	atg	ggc	tcc	att	att	ttg	ggc	gca	ggc	acg	ttt	ttg	912	
Gly	Ala	Val	Met	Met	Ala	Ser	Ile	Ile	Leu	Ala	Ala	Gly	Thr	Phe	Leu		
	290					295					300						
ggg	att	ttg	aag	ggc	ggc	ggg	atg	ttg	gac	ggc	att	tcc	aaa	gac	att	960	
Gly	Ile	Leu	Lys	Gly	Ala	Gly	Met	Leu	Asp	Ala	Ile	Ser	Lys	Asp	Ile		
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gtg	cat	atc	ctg	cgc	gac	ggc	ctg	ctg	cct	tat	ctg	cat	att	gcc	atc	1008	
Val	His	Ile	Leu	Pro	Asp	Ala	Leu	Leu	Pro	Tyr	Leu	His	Ile	Ala	Ile		
				325					330					335			
ggc	gtg	ttg	ggc	att	cgc	ctt	gag	ttg	gtt	ttg	agt	acg	gac	gct	tat	1056	
Gly	Val	Leu	Gly	Ile	Pro	Leu	Glu	Leu	Val	Leu	Ser	Thr	Asp	Ala	Tyr		
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tat	ttc	gga	ctg	ttt	cgc	att	gtg	gag	cag	att	acc	tcg	cag	ggc	ggc	1104	
Tyr	Phe	Gly	Leu	Phe	Pro	Ile	Val	Glu	Gln	Ile	Thr	Ser	Gln	Ala	Gly		
		355					360					365					
gtg	ggc	ccc	gaa	gca	gca	ggc	tat	ggc	atg	ttg	atc	ggc	agt	atc	gtc	1152	
Val	Ala	Pro	Glu	Ala	Ala	Gly	Tyr	Ala	Met	Leu	Ile	Gly	Ser	Ile	Val		
	370					375					380						
ggc	act	ttt	gtt	acg	cgc	ctt	tcg	cgc	gct	ttg	tgg	atg	ggc	ttg	ggc	1200	

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Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly
 385 390 395 400
 ttg gcg aaa ttg tgc atg ggc aaa cac atc cgt tat tgc ttt ttt tgg 1248
 Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp
 405 410 415
 gcg tgg ggt ttg tgc ctg gcg ata ttg gcc agt tgc ata gcg gca gga 1296
 Ala Trp Gly Leu Ser Leu Ala Ile Leu Ala Ser Ser Ile Ala Ala Gly
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 atc gtg cct ctg ccg taa 1314
 Ile Val Pro Leu Pro
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 <213> Neisseria meningitidis

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 Leu Phe Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu
 35 40 45
 Phe Tyr Ser Gly Gly Thr Lys Ser Val Met Gln Ile Val Ile Met Phe
 50 55 60
 Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe
 65 70 75 80
 Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val
 85 90 95
 Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp
 100 105 110
 Gly Ala Gly Ala Thr Thr Phe Leu Leu Val Val Pro Ala Leu Leu Pro
 115 120 125
 Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu
 130 135 140
 Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Trp Gly Gly Pro Thr
 145 150 155 160
 Gly Arg Val Ala Ser Val Leu Gly Ala Asp Val Gly Glu Leu Tyr Lys
 165 170 175
 Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Ala Leu
 180 185 190
 Ser Leu Leu Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu
 195 200 205

091801 E406360

Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Val Pro Leu Ser
 210 215 220

Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val
 225 230 235 240

Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro
 245 250 255

Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn
 260 265 270

Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly
 275 280 285

Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu
 290 295 300

Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Ile
 305 310 315 320

Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile
 325 330 335

Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr
 340 345 350

Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly
 355 360 365

Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val
 370 375 380

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly
 385 390 395 400

Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp
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Ala Trp Gly Leu Ser Leu Ala Ile Leu Ala Ser Ser Ile Ala Ala Gly
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Ile Val Pro Leu Pro
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act tat cag tat caa aag ccc aag ctc ttt aaa gga gcg gtt cgg aat 96
Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn
20 25 30

ctc gaa gcc gca tct tgt aaa tat atc aac gag ata tac caa cga gca 144
Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala
35 40 45

gac cca acc gca ccg ctg ttt cat ctg cgt aaa aaa ggc gca atc gtt 192
Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val
50 55 60

cct aaa gaa gaa tac gtc gaa agt ttc gac gat ttg ggc aaa act cgc 240
Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg
65 70 75 80

tac cgt ttt att aaa tcc gtt atc tac gaa cat atg aag aat ggt gcg 288
Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala
85 90 95

tcg tta gtc tat aac cat att aac aac gag ccg ttt tca gac cat atc 336
Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile
100 105 110

gcc cgt caa gtc gcc cgc ttt gcc ggc gca cat act att gtt agt gga 384
Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly
115 120 125

tat ctt gct ttt ggc agc gac gaa tct tat aaa aac cat tgg gat acc 432
Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr
130 135 140

cgc gat gtg tat gcc atc cag ctt ttc ggc aag aaa cgt tgg caa ctt 480
 Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu
 145 150 155 160

act gcc cct gat ttc cct atg cca ttg tat atg caa cag act aaa gat 528
Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp
165 170 175

act gat att tcc att cct gaa cat atc gat atg gat att atc ctt gaa 576
Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu
180 185 190

gca ggt gat gtc ctc tac atc cca cgc ggt tgg tgg cac aga cct atc 624
Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile
195 200 205

ccg ctc ggc tgt gaa acc ttc cac ttc gct gtc ggt acc ttc cag ccc 672
Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro
210 215 220

aac ggc tat aat tac ctc gag tgg cta atg aag aaa ttc ccc acg ata 720
Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile
225 230 235 240

gaa agt ctg cgc cac agt ttc tca gac tgg gag caa gat agg acg cgt 768
Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg

245	250	255	
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aac tac gaa gcc ttc agt gaa gac ttc ctc ggc aaa gaa cgc acc gat Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp 275 280 285			864
acc gct ttt cat ctc gaa cag ttc gcg aat ccc aac gct act ccg ctt Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu 290 295 300			912
tca gac gac gtc agg ttg aga cta aat gcc aat aat ttg gat acg ttg Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu 305 310 315 320			960
gaa aag gga tat ttg att ggg aat ggg atg aag ata agc gta gat gaa Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu 325 330 335			1008
ttg ggg aaa aaa gtg tta gaa cac atc ggt aag aat gaa ccg tta ttg Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu 340 345 350			1056
ttg aaa aat cta ctg gtt aac ttc aat cag gga aaa cat gaa gaa gtt Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Gly Lys His Glu Glu Val 355 360 365			1104
agg aag ttg att tat cag ttg ata gag tta gat ttt ctg gaa ctt ttg Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Leu Leu 370 375 380			1152
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 Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala
 35 40 45
 Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val
 50 55 60
 Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg
 65 70 75 80
 Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala
 85 90 95

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Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile
100 105 110

Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly
115 120 125

Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr
130 135 140

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu
145 150 155 160

Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp
165 170 175

Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu
180 185 190

Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile
195 200 205

Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro
210 215 220

Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile
225 230 235 240

Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg
245 250 255

Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val
260 265 270

Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp
275 280 285

Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu
290 295 300

Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu
305 310 315 320

Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu
325 330 335

Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu
340 345 350

Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Gly Lys His Glu Glu Val
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cgc	caa	acc	agc	ctg	acg	ggg	aaa	gtg	att	ctg	aca	cga	ccg	ttg	tca	96
Arg	Gln	Thr	Ser	Leu	Thr	Gly	Lys	Val	Ile	Leu	Thr	Arg	Pro	Leu	Ser	
			20					25					30			
ttt	tcc	cta	tgg	acg	aca	ttt	gca	tcg	ata	tct	gcg	tta	ttg	att	atc	144
Phe	Ser	Leu	Trp	Thr	Thr	Phe	Ala	Ser	Ile	Ser	Ala	Leu	Leu	Ile	Ile	
		35					40					45				
ctg	ttt	ttg	ata	ttt	ggg	aac	tat	acg	cga	aag	aca	aca	gtg	gag	gga	192
Leu	Phe	Leu	Ile	Phe	Gly	Asn	Tyr	Thr	Arg	Lys	Thr	Thr	Val	Glu	Gly	
	50					55					60					
caa	att	tta	cct	gca	tcg	ggc	gta	atc	agg	gtg	tat	gca	ccg	gat	acg	240
Gln	Ile	Leu	Pro	Ala	Ser	Gly	Val	Ile	Arg	Val	Tyr	Ala	Pro	Asp	Thr	
	65				70				75						80	
ggg	aca	att	aca	gcg	aaa	ttc	gtg	gaa	gat	gga	gaa	aag	gtt	aag	gct	288
Gly	Thr	Ile	Thr	Ala	Lys	Phe	Val	Glu	Asp	Gly	Glu	Lys	Val	Lys	Ala	
			85						90					95		
ggc	gac	aag	cta	ttt	gcg	ctt	tcg	acc	tca	cgt	ttc	ggc	gca	gga	gat	336
Gly	Asp	Lys	Leu	Phe	Ala	Leu	Ser	Thr	Ser	Arg	Phe	Gly	Ala	Gly	Asp	
			100					105					110			
agc	gtg	cag	cag	cag	ttg	aaa	acg	gag	gca	gtt	ttg	aag	aaa	acg	ttg	384
Ser	Val	Gln	Gln	Gln	Leu	Lys	Thr	Glu	Ala	Val	Leu	Lys	Lys	Thr	Leu	
		115					120					125				
gca	gaa	cag	gaa	ctg	ggg	cgt	ctg	aag	ctg	ata	cac	ggg	aat	gaa	acg	432
Ala	Glu	Gln	Glu	Leu	Gly	Arg	Leu	Lys	Leu	Ile	His	Gly	Asn	Glu	Thr	
	130					135					140					
cgc	agc	ctt	aaa	gca	act	gtc	gaa	cgt	ttg	gaa	aac	cag	aaa	ctc	cat	480
Arg	Ser	Leu	Lys	Ala	Thr	Val	Glu	Arg	Leu	Glu	Asn	Gln	Lys	Leu	His	
	145				150					155					160	
att	tcg	caa	cag	ata	gac	ggg	cag	aaa	agg	cgc	att	aga	ctt	gcg	gaa	528
Ile	Ser	Gln	Gln	Ile	Asp	Gly	Gln	Lys	Arg	Arg	Ile	Arg	Leu	Ala	Glu	
			165						170					175		
gaa	atg	ttg	cag	aaa	tat	cgt	ttc	cta	tcc	gcc	aat	gat	gca	gtg	cca	576
Glu	Met	Leu	Gln	Lys	Tyr	Arg	Phe	Leu	Ser	Ala	Asn	Asp	Ala	Val	Pro	
			180					185					190			
aaa	caa	gaa	atg	atg	aat	gtc	aag	gca	gag	ctt	tta	gag	cag	aaa	gcc	624
Lys	Gln	Glu	Met	Met	Asn	Val	Lys	Ala	Glu	Leu	Leu	Glu	Gln	Lys	Ala	
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			20					25					30		
Phe	Ser	Leu	Trp	Thr	Thr	Phe	Ala	Ser	Ile	Ser	Ala	Leu	Leu	Ile	Ile
		35					40					45			
Leu	Phe	Leu	Ile	Phe	Gly	Asn	Tyr	Thr	Arg	Lys	Thr	Thr	Val	Glu	Gly
	50					55					60				
Gln	Ile	Leu	Pro	Ala	Ser	Gly	Val	Ile	Arg	Val	Tyr	Ala	Pro	Asp	Thr
	65					70				75					80
Gly	Thr	Ile	Thr	Ala	Lys	Phe	Val	Glu	Asp	Gly	Glu	Lys	Val	Lys	Ala
				85					90					95	
Gly	Asp	Lys	Leu	Phe	Ala	Leu	Ser	Thr	Ser	Arg	Phe	Gly	Ala	Gly	Asp
			100					105					110		
Ser	Val	Gln	Gln	Gln	Leu	Lys	Thr	Glu	Ala	Val	Leu	Lys	Lys	Thr	Leu
		115					120					125			
Ala	Glu	Gln	Glu	Leu	Gly	Arg	Leu	Lys	Leu	Ile	His	Gly	Asn	Glu	Thr
	130					135					140				
Arg	Ser	Leu	Lys	Ala	Thr	Val	Glu	Arg	Leu	Glu	Asn	Gln	Lys	Leu	His
	145				150				155						160
Ile	Ser	Gln	Gln	Ile	Asp	Gly	Gln	Lys	Arg	Arg	Ile	Arg	Leu	Ala	Glu
			165					170						175	
Glu	Met	Leu	Gln	Lys	Tyr	Arg	Phe	Leu	Ser	Ala	Asn	Asp	Ala	Val	Pro
		180						185					190		
Lys	Gln	Glu	Met	Met	Asn	Val	Lys	Ala	Glu	Leu	Leu	Glu	Gln	Lys	Ala
	195					200						205			
Lys	Leu	Asp	Ala	Tyr	Arg	Arg	Glu	Glu	Val	Gly	Leu	Leu	Gln	Glu	Ile
	210					215					220				
Arg	Thr	Gln	Asn	Leu	Thr	Leu	Ala	Ser	Leu	Pro	Gln	Ala	Ala		
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aat ctg aca ttg gcc agc ctc ccc aaa cgg cat gag aca gaa caa agc 144
Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
35 40 45

cag ctt gaa cgc acc atg gcc gat att tct caa gaa gtt ttg gat ttt 192
Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
50 55 60

gaa atg cgc tct gaa caa atc atc cgt gca gga cgg tcg ggt tat ata 240
Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
65 70 75 80

gca ata ccg aac gtc gaa gtc gga cag cag gtc gat cct tcc aaa ctg 288
Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu
85 90 95

ctc ttg agc att gtt ccc gaa cgt acc gag cta tat gcc cat cta tat 336
Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr
100 105 110

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atc ccc agc agt gca gca ggc ttt atc aag ccg aaa gac aag gtt gtc      384
Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val
      115                      120                      125

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cta cgt tat cag gca tat ccc tat caa aaa ttc ggg ctt gct tcc ggc 432
Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
130 135 140

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agt gtc gta tca gta gca aaa acg gca ctg ggc aga cag gaa ttg tcg    480
Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
145                      150                      155                      160

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gga ttg ggc atg gta tcc tcc gat ttg gcg aag agc aac gaa cct gtt 528
Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
165 170 175

tat ctc gtg aaa ata aaa ccc gac aaa cca acc atc act gca tac ggt 576
Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
180 185 190

gag gaa aaa ccg ctg caa atc ggc atg acg trg gaa gca gac atc ctg 624
Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
195 200 205

cac gag aaa cgg cgg ctg tac gaa tgg gta ttg gag ctg att tat agt 672
 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser
 210 215 220

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Met Ser Gly Lys Leu
225

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 <213> Neisseria meningitidis

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 20 25 30

Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
 35 40 45

Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
 50 55 60

Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
 65 70 75 80

Ala Ile Pro Asn Val Glu Val Gly Gln Gln Val Asp Pro Ser Lys Leu
 85 90 95

Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr
 100 105 110

Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val
 115 120 125

Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
 130 135 140

Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
 145 150 155 160

Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
 165 170 175

Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
 180 185 190

Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
 195 200 205

His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Leu Ile Tyr Ser
 210 215 220

Met Ser Gly Lys Leu
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09030433 081601

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<222> (1)..(1740)

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1 5 10 15	
ccc ctt aaa acc tta gct gcc gat gaa aac gat gca gaa ctt atc cgt	96
Pro Leu Lys Thr Leu Ala Ala Asp Glu Asn Asp Ala Glu Leu Ile Arg	
20 25 30	
tcc atg cag cgt cag cag cac ata gat gct gaa ttg tta act gat gca	144
Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala	
35 40 45	
aat gtc cgt ttc gag caa cca ttg gag aag aac aat tat gtc ctg agt	192
Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser	
50 55 60	
gaa gat gaa aca ccg tgt act cgg gta aat tac att agt tta gat gat	240
Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp	
65 70 75 80	
aag acg gcg cgc aaa ttt tct ttt ctt cct tct gtg ctc atg aaa gaa	288
Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu	
85 90 95	
aca gct ttt aaa act ggg atg tgt tta ggt tcc aat aat ttg agc agg	336
Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg	
100 105 110	
cta caa aaa gcc gcg caa cag ata ctg att gtg cgt ggc tac ctc act	384
Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr	
115 120 125	
tcc caa gct att atc caa cca cag aat atg gat tcg gga att ctg aaa	432
Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys	
130 135 140	
tta cgg gta tca gca ggc gaa atc agg gat atc cgc tat gaa gaa aaa	480
Leu Arg Val Ser Ala Gly Glu Ile Arg Asp Ile Arg Tyr Glu Glu Lys	
145 150 155 160	
cgg gat gcg aag tct gcc gag ggc agt att agt gca ttc aat aac aaa	528
Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys	
165 170 175	
ctt ccc tta tat agg aac aaa att ctc aat ctt cgc gat gta gag cag	576

0930433-081501

Leu	Pro	Leu	Tyr	Arg	Asn	Lys	Ile	Leu	Asn	Leu	Arg	Asp	Val	Glu	Gln	
180							185			190						
ggc	ttg	gaa	aac	ctg	cgt	cgt	ttg	ccg	agt	gtt	aaa	aca	gat	att	cag	624
Gly	Leu	Glu	Asn	Leu	Arg	Arg	Leu	Pro	Ser	Val	Lys	Thr	Asp	Ile	Gln	
195							200			205						
att	ata	ccg	tcc	gaa	gaa	gaa	ggc	aaa	agc	gat	tta	cag	atc	aaa	tgg	672
Ile	Ile	Pro	Ser	Glu	Glu	Glu	Gly	Lys	Ser	Asp	Leu	Gln	Ile	Lys	Trp	
210							215			220						
cag	cag	aat	aaa	ccc	ata	cgg	ttc	agt	atc	ggc	ata	gat	gat	gcg	ggc	720
Gln	Gln	Asn	Lys	Pro	Ile	Arg	Phe	Ser	Ile	Gly	Ile	Asp	Asp	Ala	Gly	
225							230			235					240	
ggc	aaa	acg	acc	ggc	aaa	tat	caa	gga	aat	gtc	gct	tta	tcg	tcc	gat	768
Gly	Lys	Thr	Thr	Gly	Lys	Tyr	Gln	Gly	Asn	Val	Ala	Leu	Ser	Ser	Asp	
245							250			255						
aac	cct	ttg	ggc	tta	agc	gat	tcg	ttt	tat	gtt	tca	tat	gga	cgc	ggc	816
Asn	Pro	Leu	Gly	Leu	Ser	Asp	Ser	Phe	Tyr	Val	Ser	Tyr	Gly	Arg	Gly	
260							265			270						
ttg	gtg	cac	aaa	acg	gac	ttg	act	gct	gcc	acc	ggc	acg	gaa	act	gaa	864
Leu	Val	His	Lys	Thr	Asp	Leu	Thr	Ala	Ala	Thr	Gly	Thr	Glu	Thr	Glu	
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agc	gga	tcc	aga	agt	tac	agc	gtg	cat	tat	tcg	gtg	ccc	gta	aaa	aaa	912
Ser	Gly	Ser	Arg	Ser	Tyr	Ser	Val	His	Tyr	Ser	Val	Pro	Val	Lys	Lys	
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tggt	ctg	ttt	tct	ttt	aat	cac	aat	gga	cat	cgt	tac	cac	gaa	gca	acc	960
Trp	Leu	Phe	Ser	Phe	Asn	His	Asn	Gly	His	Arg	Tyr	His	Glu	Ala	Thr	
305							310			315					320	
gaa	ggc	tat	tcc	gtc	aat	tac	gat	tac	aac	ggc	aaa	caa	tat	cag	agc	1008
Glu	Gly	Tyr	Ser	Val	Asn	Tyr	Asp	Tyr	Asn	Gly	Lys	Gln	Tyr	Gln	Ser	
325							330			335						
agc	ctg	gcc	gcc	gag	cgc	atg	ctt	tgg	ccc	ccc	agc	ttt	cct	caa	act	1056
Ser	Leu	Ala	Ala	Glu	Arg	Met	Leu	Trp	Pro	Pro	Ser	Phe	Pro	Gln	Thr	
340							345			350						
tca	gtc	cga	atg	aaa	tta	tgg	aca	cgc	caa	acc	tat	aaa	tac	atc	gac	1104
Ser	Val	Arg	Met	Lys	Leu	Trp	Thr	Arg	Gln	Thr	Tyr	Lys	Tyr	Ile	Asp	
355							360			365						
gat	gcc	gaa	atc	gaa	gtg	caa	cgc	cgc	cgc	tct	gca	ggc	tgg	gaa	gcc	1152
Asp	Ala	Glu	Ile	Glu	Val	Gln	Arg	Arg	Arg	Ser	Ala	Gly	Trp	Glu	Ala	
370							375			380						
gaa	ttg	cgc	cac	cgt	gct	tac	ctc	cac	cgt	tgg	cag	ctt	gac	ggc	aag	1200
Glu	Leu	Arg	His	Arg	Ala	Tyr	Leu	His	Arg	Trp	Gln	Leu	Asp	Gly	Lys	
385							390			395					400	
ttg	tct	tac	aaa	cgc	ggg	acc	ggc	atg	cgc	caa	agt	atg	ccc	gca	cct	1248
Leu	Ser	Tyr	Lys	Arg	Gly	Thr	Gly	Met	Arg	Gln	Ser	Met	Pro	Ala	Pro	
405							410			415						
gaa	gaa	aac	ggc	ggc	ggt	act	att	cca	gcc	aca	tcc	cgt	atg	aaa	atc	1296

Glu Glu Asn Gly Gly Gly Thr Ile Pro Ala Thr Ser Arg Met Lys Ile
420 425 430

ata acc gcc gga ttg gat gca gcg gcc ccg tct atg ttg ggc aaa cag 1344
Ile Thr Ala Gly Leu Asp Ala Ala Ala Pro Ser Met Leu Gly Lys Gln
435 440 445

cag ttt ttc tac gca acc gcc att caa gct caa tgg aac aaa acg cct 1392
Gln Phe Phe Tyr Ala Thr Ala Ile Gln Ala Gln Trp Asn Lys Thr Pro
450 455 460

ttg gtt gcc caa gac aag ttg tct atc ggc agc cgc tac acc gtt cgc 1440
Leu Val Ala Gln Asp Lys Leu Ser Ile Gly Ser Arg Tyr Thr Val Arg
465 470 475 480

gga ttt gat ggg gag cag agt ctt ttc gga gag cga ggt ttc tac tgg 1488
Gly Phe Asp Gly Glu Gln Ser Leu Phe Gly Glu Arg Gly Phe Tyr Trp
485 490 495

cag aat act tta act tgg tat ttt cat ccg aac cat cag ttc tat ctc 1536
Gln Asn Thr Leu Thr Trp Tyr Phe His Pro Asn His Gln Phe Tyr Leu
500 505 510

ggt gcg gac tat ggc cgc gta tct ggc gaa agt gca caa tat gta tcg 1584
Gly Ala Asp Tyr Gly Arg Val Ser Gly Glu Ser Ala Gln Tyr Val Ser
515 520 525

ggc aag cag ctg atg ggt gca gtg gtc ggc ttc aga gga ggg cat aaa 1632
Gly Lys Gln Leu Met Gly Ala Val Val Gly Phe Arg Gly Gly His Lys
530 535 540

gta ggc ggt atg ttt gct tat gat ctg ttt gcc ggc aag ccg ctt cat 1680
Val Gly Gly Met Phe Ala Tyr Asp Leu Phe Ala Gly Lys Pro Leu His
545 550 555 560

aaa ccc aaa ggc ttt cag acg acc aac acc gtt tac ggc ttc aac ttg 1728
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565 570 575

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Asn Tyr Ser Phe
580

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Ser Met Gln Arg Gln Gln His Ile Asp Ala Glu Leu Leu Thr Asp Ala
35 40 45

Asn Val Arg Phe Glu Gln Pro Leu Glu Lys Asn Asn Tyr Val Leu Ser

009400 000000

50	55	60
Glu Asp Glu Thr Pro Cys Thr Arg Val Asn Tyr Ile Ser Leu Asp Asp 65 70 75 80		
Lys Thr Ala Arg Lys Phe Ser Phe Leu Pro Ser Val Leu Met Lys Glu 85 90 95		
Thr Ala Phe Lys Thr Gly Met Cys Leu Gly Ser Asn Asn Leu Ser Arg 100 105 110		
Leu Gln Lys Ala Ala Gln Gln Ile Leu Ile Val Arg Gly Tyr Leu Thr 115 120 125		
Ser Gln Ala Ile Ile Gln Pro Gln Asn Met Asp Ser Gly Ile Leu Lys 130 135 140		
Leu Arg Val Ser Ala Gly Glu Ile Arg Asp Ile Arg Tyr Glu Glu Lys 145 150 155 160		
Arg Asp Ala Lys Ser Ala Glu Gly Ser Ile Ser Ala Phe Asn Asn Lys 165 170 175		
Leu Pro Leu Tyr Arg Asn Lys Ile Leu Asn Leu Arg Asp Val Glu Gln 180 185 190		
Gly Leu Glu Asn Leu Arg Arg Leu Pro Ser Val Lys Thr Asp Ile Gln 195 200 205		
Ile Ile Pro Ser Glu Glu Glu Gly Lys Ser Asp Leu Gln Ile Lys Trp 210 215 220		
Gln Gln Asn Lys Pro Ile Arg Phe Ser Ile Gly Ile Asp Asp Ala Gly 225 230 235 240		
Gly Lys Thr Thr Gly Lys Tyr Gln Gly Asn Val Ala Leu Ser Ser Asp 245 250 255		
Asn Pro Leu Gly Leu Ser Asp Ser Phe Tyr Val Ser Tyr Gly Arg Gly 260 265 270		
Leu Val His Lys Thr Asp Leu Thr Ala Ala Thr Gly Thr Glu Thr Glu 275 280 285		
Ser Gly Ser Arg Ser Tyr Ser Val His Tyr Ser Val Pro Val Lys Lys 290 295 300		
Trp Leu Phe Ser Phe Asn His Asn Gly His Arg Tyr His Glu Ala Thr 305 310 315 320		
Glu Gly Tyr Ser Val Asn Tyr Asp Tyr Asn Gly Lys Gln Tyr Gln Ser 325 330 335		
Ser Leu Ala Ala Glu Arg Met Leu Trp Pro Pro Ser Phe Pro Gln Thr 340 345 350		
Ser Val Arg Met Lys Leu Trp Thr Arg Gln Thr Tyr Lys Tyr Ile Asp 355 360 365		
Asp Ala Glu Ile Glu Val Gln Arg Arg Arg Ser Ala Gly Trp Glu Ala		

003043-01601

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<213> Neisseria meningitidis
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ctt ttg ctt gtg tgg acg tgc ggt tac cga tac gcc gcc gac aag gcc 96
Leu Leu Leu Val Trp Thr Cys Gly Tyr Arg Tyr Ala Ala Asp Lys Ala
20 25 30
gaa gcg aaa caa acc gcc ctg att gcc acc tat cgg cat tct tct atg 144
Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met
35 40 45
gtt gcg gcg gaa caa tac gcc ttg cag ctt aaa aaa gcg cag gac gaa 192
Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu
50 55 60
agg cag cgg tgg tac gac ttt toc caa aaa caa gga aga aag ccc gtg 240
Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val
65 70 75 80
aaa aaa cag tat ccg ccg caa acg aaa aaa gcc ggc tat ctg aaa acc 288
Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr
85 90 95
aag gaa gaa ctg ctt gcg gaa ttg gct tgc ctt aaa gcg gaa atg gct 336
Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala
100 105 110
gcc cta aaa aag ctc gat gcc tta atc tat ggg aaa gaa gtg cgg cag 384
Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln
115 120 125
aaa gaa cgc aac tcg tcg cag ggt taa 411
Lys Glu Arg Asn Ser Ser Gln Gly
130 135

<210> 22
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<212> PRT
<213> Neisseria meningitidis

09030433.081601

<400> 22

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20 25 30

Glu Ala Lys Gln Thr Ala Leu Ile Ala Thr Tyr Arg His Ser Ser Met
35 40 45

Val Ala Ala Glu Gln Tyr Ala Leu Gln Leu Lys Lys Ala Gln Asp Glu
50 55 60

Arg Gln Arg Trp Tyr Asp Phe Ser Gln Lys Gln Gly Arg Lys Pro Val
65 70 75 80

Lys Lys Gln Tyr Pro Pro Gln Thr Lys Lys Ala Gly Tyr Leu Lys Thr
85 90 95

Lys Glu Glu Leu Leu Ala Glu Leu Ala Cys Leu Lys Ala Glu Met Ala
100 105 110

Ala Leu Lys Lys Leu Asp Ala Leu Ile Tyr Gly Lys Glu Val Arg Gln
115 120 125

Lys Glu Arg Asn Ser Ser Gln Gly
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<210> 23

<211> 924

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<213> Neisseria meningitidis

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<222> (1) .. (921)

003043-081501

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aat aat ttc ggg ttt ttg cgc ctg ccg ctt aat ttt atg ccg tat gaa 96
Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu
20 25 30

agt cat gcc gat tgg gtt att acc ggc gtg cct tat gat atg gcg gtt 144
Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val
35 40 45

tca ggg cgt tcc ggc gcg cgt ttc ggt cct gaa gcc atc cgg cgc gcc 192
Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
50 55 60

tcc gtc aac ctc gct tgg gag cac cgc agg ttt cca tgg aca ttt gat 240
Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
65 70 75 80

gtg cgc gaa cgc ctg aac att att gat tgc ggc gac ttg gtt ttt tct 288
Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
85 90 95

ttt ggc gac agc agg gat ttt gtc gaa aaa atg gaa gcg cac gcc gcc 336
Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly
100 105 110

aaa tta ctt tct tcc ggc aaa cgc tgt ttg agt ttg ggc ggc gac cat 384
Lys Leu Leu Ser Ser Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His
115 120 125

ttc att acc ctc ccg ttg ttg cgc gcc cac gcc cgc tat ttc ggc aaa 432
Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys
130 135 140

ctc gca ctg att cat ttt gac gcg cac acc gac acc tac gac aac gcc 480
Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly
145 150 155 160

agc gaa tac gac cac ggt acg atg ttc tat acc gcc ccc aag gaa gcc 528
Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly
165 170 175

ctc atc gac ccg tcc cgt tcc gta caa atc ggc ata cgt acc gaa cac 576

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09030433 DETE01

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Ser	Lys	Lys	Leu	Pro	Phe	Thr	Val	Leu	Thr	Ala	Pro	Gln	Val	Asn	Glu	
		195					200					205				
gac	agt	gtt	gaa	gag	acc	gtc	cgt	aaa	atc	aaa	gaa	acc	gtc	ggc	aat	672
Asp	Ser	Val	Glu	Glu	Thr	Val	Arg	Lys	Ile	Lys	Glu	Thr	Val	Gly	Asn	
		210					215				220					
atg	ccc	gtt	tac	ctg	act	ttc	gac	ata	gac	tgc	ctc	gac	ccg	tcg	ttc	720
Met	Pro	Val	Tyr	Leu	Thr	Phe	Asp	Ile	Asp	Cys	Leu	Asp	Pro	Ser	Phe	
		225				230				235					240	
gcc	ccc	ggg	acc	ggg	acg	ccc	gta	tgc	ggc	ggc	ttg	agc	agc	gac	agg	768
Ala	Pro	Gly	Thr	Gly	Thr	Pro	Val	Cys	Gly	Gly	Leu	Ser	Ser	Asp	Arg	
				245					250					255		
gca	tta	aaa	atc	cta	cgt	ggg	ctg	acg	gat	ctc	gac	atc	gtc	ggg	atg	816
Ala	Leu	Lys	Ile	Leu	Arg	Gly	Leu	Thr	Asp	Leu	Asp	Ile	Val	Gly	Met	
			260					265					270			
gat	gtt	gta	gaa	gtt	gcc	ccc	tct	tac	gac	caa	tcc	gac	att	acc	gct	864
Asp	Val	Val	Glu	Val	Ala	Pro	Ser	Tyr	Asp	Gln	Ser	Asp	Ile	Thr	Ala	
		275					280					285				
ttg	gcc	ggc	gcc	aca	att	gcc	ttg	gaa	atg	ctt	tac	ctt	caa	ggg	gcg	912
Leu	Ala	Gly	Ala	Thr	Ile	Ala	Leu	Glu	Met	Leu	Tyr	Leu	Gln	Gly	Ala	
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aaa	aag	gac	tga													924
Lys	Lys	Asp														
		305														

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 <213> Neisseria meningitidis

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 Ser His Ala Asp Trp Val Ile Thr Gly Val Pro Tyr Asp Met Ala Val
 35 40 45
 Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
 50 55 60
 Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
 65 70 75 80
 Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
 85 90 95

09030433 001604

Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly
100 105 110

Lys Leu Leu Ser Ser Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His
115 120 125

Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys
130 135 140

Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly
145 150 155 160

Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly
165 170 175

Leu Ile Asp Pro Ser Arg Ser Val Glu Ile Gly Ile Arg Thr Glu His
180 185 190

Ser Lys Lys Leu Pro Phe Thr Val Leu Thr Ala Pro Gln Val Asn Glu
195 200 205

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
210 215 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
225 230 235 240

Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg
245 250 255

Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met
260 265 270

Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
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290 295 300

Lys Lys Asp
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<212> DNA
<213> Neisseria meningitidis

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<221> CDS
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09830433-08160

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1 5 10 15

gaa tat ttt gtc gta tgc ttt ctg cgt ttg atg cca ctc tct ccg tgt 144
Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys
35 40 45

aat ctg tat ttt gtc acc cat ctg cgt acc aat gaa tcg gaa ata gaa 192
Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu
50 55 60

aga tgg tct gct gtt ccc tgc caa ata gta ttg aac gac ggc aag tcg 240
Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser
65 70 75 80

gaa ttc ggc gga ttc gca ttt gaa gtg caa ctt tcc cta aca gaa aaa 288
Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys
85 90 95

ggc cag tat ggc gta gca tac gac ctt tcc tgc aag aaa gat tgc cat 336
Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His
100 105 110

gag cta cac gca act gac cca agg cga acg ata cca cat cca ata cct 384
Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro
115 120 125

gtc cgc cca ctg cac cgt cac cga aat cgc caa aca gct taa 426
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130 135 140

<210> 26

<211> 141

<212> PRT

<213> Neisseria meningitidis

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Ile Pro Tyr Pro Val Thr Arg Arg Ile Ala Ser Ser Leu Tyr Ser Thr
20 25 30

Glu Tyr Phe Val Val Cys Phe Leu Arg Leu Met Pro Leu Ser Pro Cys
35 40 45

Asn Leu Tyr Phe Val Thr His Leu Arg Thr Asn Glu Ser Glu Ile Glu
50 55 60

Arg Trp Ser Ala Val Pro Cys Gln Ile Val Leu Asn Asp Gly Lys Ser
65 70 75 80

Glu Phe Gly Gly Phe Ala Phe Glu Val Gln Leu Ser Leu Thr Glu Lys
85 90 95

Gly Gln Tyr Ala Val Ala Tyr Asp Leu Ser Cys Lys Lys Asp Cys His
100 105 110

Glu Leu His Ala Thr Asp Pro Arg Arg Thr Ile Pro His Pro Ile Pro
115 120 125

Val Pro Pro Leu His Arg His Arg Asn Arg Gln Thr Ala
130 135 140

<210> 27

<211> 351

<212> DNA

<213> Neisseria meningitidis

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<221> CDS

<222> (1) .. (348)

093043-03401

atg caa aac ggc ggg gga aag att tac cag acg gcg gac aat gtg gaa 48
Met Gln Asn Gly Gly Gly Lys Ile Tyr Gln Thr Ala Asp Asn Val Glu
1 5 10 15

ggg att atg ctg ttg aag gta gta cct gag cgt acc gtt tcg gca gat 96
Gly Ile Met Leu Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp
20 25 30

gca aaa acc aga gac ccg atg tgg gac aat gcg gct tta cag acc agc 144
Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser
35 40 45

gaa ggc gta aat ttt att gct cgt ttc cta gga ttt ttt agc gat ggg 192
Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly
50 55 60

gaa tac cgc tac gtg gat gtc ctg caa ccc aac cat tcc gat att att 240
Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile
65 70 75 80

cgg tat tca ggt aaa gat ttt ccg cta aat caa ata ctt aac cat ata 288
Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile
85 90 95

cac ccc gcc cgt tat gcg gta acg ttc gaa aac aat gtc gat tcc aag 336
His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys
 100 105 110

ctg cgc agg cac tga 351
Leu Arg Arg His
115

<211> 116

<212> PRT

<213> Neisseria meningitidis

<400> 28

Met Gln Asn Gly Gly Gly Lys Ile Tyr Gln Thr Ala Asp Asn Val Glu
1 5 10 15

Gly Ile Met Leu Leu Lys Val Val Pro Glu Arg Thr Val Ser Ala Asp
20 25 30

Ala Lys Thr Arg Asp Pro Met Trp Asp Asn Ala Ala Leu Gln Thr Ser
 35 40 45
 Glu Gly Val Asn Phe Ile Ala Arg Phe Leu Gly Phe Phe Ser Asp Gly
 50 55 60
 Glu Tyr Arg Tyr Val Asp Val Leu Gln Pro Asn His Ser Asp Ile Ile
 65 70 75 80
 Arg Tyr Ser Gly Lys Asp Phe Pro Leu Asn Gln Ile Leu Asn His Ile
 85 90 95
 His Pro Ala Arg Tyr Ala Val Thr Phe Glu Asn Asn Val Asp Ser Lys
 100 105 110
 Leu Arg Arg His
 115

<210> 29
 <211> 1404
 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> CDS
 <222> (1)..(1401)

<400> 29
 atg aca ttg ctc aat cta atg ata atg caa gat tac ggt att tcc gtt 48
 Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
 1 5 10 15
 tgc ctg aca ctg acg ccc tat ttg caa cat gaa cta ttt tcg gct atg 96
 Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
 20 25 30
 aaa tcc tat ttt tcc aaa tat atc cta ccc gtt tca ctt ttt acc ttg 144
 Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
 35 40 45
 cca cta tcc ctt tcc cca tcc gtt tcg gct ttt acg ctg cct gaa gca 192
 Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
 50 55 60
 tgg cgg gcg gcg cag caa cat tcg gct gat ttt caa gcg tcc cat tac 240
 Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
 65 70 75 80
 cag cgt gat gca gtg cgc gca cgg caa caa caa gcc aag gcc gca ttc 288
 Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
 85 90 95
 ctt ccc cat gta tcc gcc aat gcc agc tac cag cgc cag ccg cca tcg 336
 Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
 100 105 110
 att tct tcc acc cgc gaa aca cag gga tgg agc gtg cag gtg gga caa 384

009043 009043

Ile	Ser	Thr	Arg	Glu	Thr	Gln	Gly	Trp	Ser	Val	Gln	Val	Gly	Gln			
115					120					125							
acc	tta	ttt	gac	gct	gcc	aaa	ttt	gca	caa	tac	cgc	caa	agc	agg	ttc	432	
Thr	Leu	Phe	Asp	Ala	Ala	Lys	Phe	Ala	Gln	Tyr	Arg	Gln	Ser	Arg	Phe		
130					135					140							
gat	acg	cag	gct	gca	gaa	cag	cgt	ttc	gat	gcg	gca	cgc	gaa	gaa	ttg	480	
Asp	Thr	Gln	Ala	Ala	Glu	Gln	Arg	Phe	Asp	Ala	Ala	Arg	Glu	Glu	Leu		
145					150					155					160		
ctg	ttg	aaa	gtt	gcc	gaa	agt	tat	ttc	aac	gtt	tta	ctc	agc	cga	gac	528	
Leu	Leu	Lys	Val	Ala	Glu	Ser	Tyr	Phe	Asn	Val	Leu	Leu	Ser	Arg	Asp		
165					170					175							
acc	gtt	gcc	gcc	cat	gcg	gcg	gaa	aaa	gag	gct	tat	gcc	cag	cag	gta	576	
Thr	Val	Ala	Ala	His	Ala	Ala	Glu	Lys	Glu	Ala	Tyr	Ala	Gln	Gln	Val		
180					185					190							
agg	cag	gcg	cag	gct	tta	ttc	aat	aaa	ggt	gct	gcc	acc	gcg	ctg	gat	624	
Arg	Gln	Ala	Gln	Ala	Leu	Phe	Asn	Lys	Gly	Ala	Ala	Thr	Ala	Leu	Asp		
195					200					205							
att	cac	gaa	gcc	aaa	gcc	ggt	tac	gac	aat	gcc	ctg	gcc	caa	gaa	atc	672	
Ile	His	Glu	Ala	Lys	Ala	Gly	Tyr	Asp	Asn	Ala	Leu	Ala	Gln	Glu	Ile		
210					215					220							
gcc	gta	ttg	gct	gag	aaa	caa	acc	tat	gaa	aac	cag	ttg	aac	gac	tac	720	
Ala	Val	Leu	Ala	Glu	Lys	Gln	Thr	Tyr	Glu	Asn	Gln	Leu	Asn	Asp	Tyr		
225					230					235					240		
acc	gac	ctg	gat	agc	aaa	caa	atc	gag	gcc	ata	gat	acc	gcc	aac	ctg	768	
Thr	Asp	Leu	Asp	Ser	Lys	Gln	Ile	Glu	Ala	Ile	Asp	Thr	Ala	Asn	Leu		
245					250					255							
ttg	gca	cgc	tat	ctg	ccc	aag	ctg	gaa	cgt	tac	agt	ctg	gat	gaa	tgg	816	
Leu	Ala	Arg	Tyr	Leu	Pro	Lys	Leu	Glu	Arg	Tyr	Ser	Leu	Asp	Glu	Trp		
260					265					270							
cag	cgc	att	gcc	tta	tcc	aac	aat	cat	gaa	tac	cgg	atg	cag	cag	ctt	864	
Gln	Arg	Ile	Ala	Leu	Ser	Asn	Asn	His	Glu	Tyr	Arg	Met	Gln	Gln	Leu		
275					280					285							
gcc	ctg	caa	agc	agc	gga	cag	gcg	ctt	cgg	gca	gca	cag	aac	agc	cgc	912	
Ala	Leu	Gln	Ser	Ser	Gly	Gln	Ala	Leu	Arg	Ala	Ala	Gln	Asn	Ser	Arg		
290					295					300							
tat	ccc	acc	gtt	tct	gcc	cat	gtc	ggc	tat	cag	aat	aac	ctc	tac	act	960	
Tyr	Pro	Thr	Val	Ser	Ala	His	Val	Gly	Tyr	Gln	Asn	Asn	Leu	Tyr	Thr		
305					310					315					320		
tca	tct	gcg	cag	aat	aat	gac	tac	cac	tat	cgg	ggc	aaa	ggg	atg	agc	1008	
Ser	Ser	Ala	Gln	Asn	Asn	Asp	Tyr	His	Tyr	Arg	Gly	Lys	Gly	Met	Ser		
325					330					335							
gtc	ggc	gta	cag	ttg	aat	ttg	ccg	ctt	tat	acc	ggc	gga	gaa	ttg	tcg	1056	
Val	Gly	Val	Gln	Leu	Asn	Leu	Pro	Leu	Tyr	Thr	Gly	Gly	Glu	Leu	Ser		
340					345					350							
ggc	aaa	atc	cat	gaa	gcc	gaa	gcg	caa	tac	ggg	gcc	gcc					

ctg acc gca acc gag cgg cac atc aaa ctc gcc gta cgc cag gct tat	1152
Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr	
370 375 380	
acc gaa agc ggt gcg gcg cgt tac caa atc atg gcg caa gaa cgg gtt	1200
Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val	
385 390 395 400	
ttg gaa agc agc cgt ttg aaa ctg aaa tcg acc gaa acc ggc caa caa	1248
Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln	
405 410 415	
tac ggc atc cgc aac cgg ctg gaa gta ata cgg gcg cgg cag gaa gtc	1296
Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val	
420 425 430	
gcc caa gca gaa cag aaa ctg gct caa gca cgg tac aaa ttc atg ctg	1344
Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu	
435 440 445	
gct tat ttg cgc ttg gtg aaa gag agc ggg tta ggg ttg gaa acg gta	1392
Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val	
450 455 460	
ttt gcg gaa taa	1404
Phe Ala Glu	
465	

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<210> 30
<211> 467
<212> PRT
<213> Neisseria meningitidis
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<400> 30
Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
  1          5          10          15
Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
      20          25          30
Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu
      35          40          45
Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala
      50          55          60
Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr
      65          70          75          80
Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe
      85          90          95
Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser
      100          105          110
Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln

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115	120	125
Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe 130 135 140		
Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu 145 150 155 160		
Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp 165 170 175		
Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val 180 185 190		
Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp 195 200 205		
Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile 210 215 220		
Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr 225 230 235 240		
Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu 245 250 255		
Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp 260 265 270		
Gln Arg Ile Ala Leu Ser Asn Asn His Glu Tyr Arg Met Gln Gln Leu 275 280 285		
Ala Leu Gln Ser Ser Gly Gln Ala Leu Arg Ala Ala Cln Asn Ser Arg 290 295 300		
Tyr Pro Thr Val Ser Ala His Val Gly Tyr Gln Asn Asn Leu Tyr Thr 305 310 315 320		
Ser Ser Ala Gln Asn Asn Asp Tyr His Tyr Arg Gly Lys Gly Met Ser 325 330 335		
Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser 340 345 350		
Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln 355 360 365		
Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr 370 375 380		
Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val 385 390 395 400		
Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln 405 410 415		
Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val 420 425 430		
Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu		

00000433-081504

435 440 445
Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
450 455 460

Phe Ala Glu
465

<210> 31
<211> 696
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(693)

<400> 31
atg aaa caa tcc gcc cga ata aaa aat atg gat cag aca tta aaa aat 48
Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn
1 5 10 15
aca ttg ggc att tgc ggc ctt tta gcc ttt tgt ttt ggc ggc gcc atc 96
Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
20 25 30
gca tca ggc tat cac ttg gaa tac gaa tac ggc tac cgt tat tct gcc 144
Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala
35 40 45
gtg ggt gct ttg gct tgg gtt gta ttt tta tta tta ttg gca cgt ggt 192
Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly
50 55 60
ttc ccc cgc gct tct tca gtc gtt tta ctg att tac gtc ggc aca acc 240
Phe Pro Arg Val Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr
65 70 75 80
gcc cta tat ttg ccc gtc gcc tgg ctg tat ggt ggc ccc tct tat cag 288
Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln
85 90 95
ata gtc ggt tcc ata ttg gaa agc aat cct gcc gag ggc cgt gaa ttt 336
Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe
100 105 110
gtc gcc aat ctt ccc ggc tgg ctt tat ttt gtg cag gca tta ttt ttc 384
Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe
115 120 125
att ttt ggc ttg aca gtt tgg aga tat tgt gta tcc ggg ggg gta ttt 432
Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe
130 135 140
gct gac gta aaa aac tat aaa cgc cgc agc aaa ata tgg ctg act ata 480
Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile
145 150 155 160

090437.08460

tta ttg act ttg att ttg tcc tgc gcg gtg atg gat aaa atc gcc agc 528
 Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser
 165 170 175

gat aaa gat ttg cga gaa cct gat gcc ggc ctg ttg ttg aat att ttc 576
 Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe
 180 185 190

gac ctg tat tac gat ttg gct tcc gcg ccg gca cca ata tgt cgc caa 624
 Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln
 195 200 205

gcg cgc cca cat ttt gga agc agc aaa aaa agc gtc aac atg gca tat 672
 Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr
 210 215 220

ccg tca tgt tgc gcc caa gta taa 696
 Pro Ser Cys Cys Ala Gln Val
 225 230

<210> 32
 <211> 231
 <212> PRT
 <213> Neisseria meningitidis

<400> 32
 Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn
 1 5 10 15

Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
 20 25 30

Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala
 35 40 45

Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly
 50 55 60

Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr
 65 70 75 80

Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln
 85 90 95

Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe
 100 105 110

Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe
 115 120 125

Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe
 130 135 140

Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile
 145 150 155 160

Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser
 165 170 175

003043 003043

Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe
 180 185 190
 Asp Leu Tyr Tyr Asp Leu Ala Ser Ala Pro Ala Pro Ile Cys Arg Gln
 195 200 205
 Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr
 210 215 220
 Pro Ser Cys Cys Ala Gln Val
 225 230

<210> 33
 <211> 909
 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> CDS
 <222> (1) .. (906)

<400> 33
 atg aat gtt tac ggt ttc cca ttg ccc gat acg cct ttt ttg agt cgg 48
 Met Asn Val Tyr Gly Phe Pro Leu Pro Asp Thr Pro Phe Leu Ser Arg
 1 5 10 15
 acc aaa ggg ctg ttg ata aac ggt tac cat ttc acc gcc cac gcg acg 96
 Thr Lys Gly Leu Leu Ile Asn Gly Tyr His Phe Thr Ala His Ala Thr
 20 25 30
 aat ctt tgg ctg ccg cag act ttg ggg ctg cgg gga gag ccg aac aat 144
 Asn Leu Ser Leu Pro Gln Thr Leu Gly Leu Pro Gly Glu Pro Asn Asn
 35 40 45
 aac att gtc agc ttg gcc aag cag gcc ggt ttt cgg acg gcc tgg ctg 192
 Asn Ile Val Ser Leu Ala Lys Gln Ala Gly Phe Arg Thr Ala Trp Leu
 50 55 60
 tct aat caa gga atg ttg ggg cat ttt gcc aac gaa att tcc acc tat 240
 Ser Asn Gln Gly Met Leu Gly His Phe Ala Asn Glu Ile Ser Thr Tyr
 65 70 75 80
 gcc cta cgc agc gat tat ccg tgg ttt acc caa agg ggt gat tat gcc 288
 Ala Leu Arg Ser Asp Tyr Pro Trp Phe Thr Gln Arg Gly Asp Tyr Gly
 85 90 95
 aaa agc gcc ggg ttg agc gat cgc ctt ttg ttg ccg gcc ttc aaa cgg 336
 Lys Ser Ala Gly Leu Ser Asp Arg Leu Leu Leu Pro Ala Phe Lys Arg
 100 105 110
 gtt ttg ata gga aat gca gcc acg aag cct cgg ctg att gtg atg cac 384
 Val Leu Ile Gly Asn Ala Gly Thr Lys Pro Arg Leu Ile Val Met His
 115 120 125
 ctg atg ggt tgg cac agt gat ttt tgc aca cgt ttg gat aag gat gcc 432
 Leu Met Gly Ser His Ser Asp Phe Cys Thr Arg Leu Asp Lys Asp Ala
 130 135 140

099780" E40E860

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<210> 34
<211> 302
<212> PRT
<213> Neisseria meningitidis
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<400> 34
Met Asn Val Tyr Gly Phe Pro Leu Pro Asp Thr Pro Phe Leu Ser Arg
  1             5             10             15
Thr Lys Gly Leu Leu Ile Asn Gly Tyr His Phe Thr Ala His Ala Thr
      20             25             30
Asn Leu Ser Leu Pro Gln Thr Leu Gly Leu Pro Gly Glu Pro Asn Asn
      35             40             45
Asn Ile Val Ser Leu Ala Lys Gln Ala Gly Phe Arg Thr Ala Trp Leu
      50             55             60
Ser Asn Gln Gly Met Leu Gly His Phe Ala Asn Glu Ile Ser Thr Tyr

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65		70		75		80
Ala Leu Arg Ser Asp Tyr Pro Trp Phe Thr Gln Arg Gly Asp Tyr Gly						
	85			90		95
Lys Ser Ala Gly Leu Ser Asp Arg Leu Leu Leu Pro Ala Phe Lys Arg						
	100		105			110
Val Leu Ile Gly Asn Ala Gly Thr Lys Pro Arg Leu Ile Val Met His						
	115		120			125
Leu Met Gly Ser His Ser Asp Phe Cys Thr Arg Leu Asp Lys Asp Ala						
	130		135			140
Arg Arg Phe Gln Tyr Gln Thr Glu Lys Ile Ser Cys Tyr Val Ser Thr						
	145		150		155	160
Ile Ala Gln Thr Asp Lys Phe Leu Glu Asp Thr Val Lys Ile Leu Asn						
		165		170		175
Glu Asn Lys Glu Ser Trp Ser Leu Val Tyr Phe Ser Asp His Gly Leu						
		180		185		190
Met His Val Gly Lys Gly Gly Glu Arg Thr Leu Thr His Gly Ala Trp						
	195		200			205
Lys Arg Gln Ser Tyr Gly Val Pro Leu Val Lys Ile Ser Ser Asp Asp						
	210		215			220
Thr Arg Arg Glu Met Ile Lys Val Arg Arg Ser Ala Phe Asn Phe Leu						
	225		230		235	240
Arg Gly Phe Gly Ser Trp Thr Gly Ile Glu Thr Asp Glu Leu Pro Asp						
		245		250		255
Asp Gly Tyr Asp Phe Trp Gly Asn Val Pro Asp Val Gln Gly Glu Gly						
	260		265			270
Asn Asn Leu Ala Phe Ile Asp Gly Leu Pro Asp Asp Pro Ala Pro Trp						
	275		280			285
Tyr Ala Gly Lys Gly Lys Ser Thr Lys Asn Thr Ser Lys Lys						
	290		295			300

<210> 35
 <211> 864
 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> CDS
 <222> (1)..(861)

0930433.081601

<400> 35

atg atg agt caa cac tct gcc gga gca cgt ttc cgc caa gcc gtg aaa 48
Met Met Ser Gln His Ser Ala Gly Ala Arg Phe Arg Gln Ala Val Lys
1 5 10 15

gaa tcg aat ccg ctt gcc gtc gcc ggt tgc gtc aat gct tat ttt gca 96
Glu Ser Asn Pro Leu Ala Val Ala Gly Cys Val Asn Ala Tyr Phe Ala
20 25 30

cga ttg gcc acc caa agc ggt ttc aaa gcc atc tat ctg tcc ggc ggc 144
Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly
35 40 45

ggc gtg gca gcc tgt tct tgc ggt atc cct gat ttg ggc att acc aca 192
Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr
50 55 60

atg gaa gat gtg ctg atc gac gca cga cgc att acg gac aac gtg gat 240
Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp
65 70 75 80

acg cct ctg ctg gtg gac atc gat gtg ggt tgg ggc ggt gca ttc aat 288
Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn
85 90 95

att gcc cgt acc att cgc aac ttc gaa cgc gcc ggt gtt gca gcg gtc 336
Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Ala Val
100 105 110

cac atc gaa gat cag gta gcg caa aaa cgc tgc ggc cac cgt ccg aac 384
His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn
115 120 125

aaa gcc att gta tct aaa gat gaa atg gtc gac cgt atc aaa gct gcc 432
Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala
130 135 140

gta gat gcg cgc gtt gat gag aac ttc gag att atg gcg cgt acc gat 480
Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp
145 150 155 160

gcg ctg gcg gta gaa ggt ttg gat gcc gct acc gaa cgc gcc caa gct 528
Ala Leu Ala Val Glu Gly Leu Asp Ala Ala Ile Glu Arg Ala Gln Ala
165 170 175

tgt gtc gaa gcc ggt gcg gac atg att ttc cct gaa gcc atg acc gat 576
Cys Val Glu Ala Gly Ala Asp Met Ile Phe Pro Glu Ala Met Thr Asp
180 185 190

ttg aac atg tac cgc caa tct gca gat gcg gtg aaa gtg ccc gtg ttg 624
Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu
195 200 205

gcg aac att acc gag ttt ggt tct acc cgc ctt tat acc caa agc gag 672
Ala Asn Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu
210 215 220

ctg gct gaa aac ggc gtg tgg ctg gtg ctg tat ccg ctg tca tcg ttc 720
Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe
225 230 235 240

cgt gca gca agc aaa gcc gct ctg aat gtt tac gaa gcg att atg cgc 768
Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg
245 250 255

00330433 004604

gat ggc act tca ggc ggc ggt ggt gga cag tat gca aac ccg tgc cga 816
Asp Gly Thr Ser Gly Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg
260 265 270

gct gta cga gca tct gaa cta tca tgc ctt cga gca aaa act gga taa 864
Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly
275 280 285

<210> 36

<211> 287

<212> PRT

<213> Neisseria meningitidis

<400> 36

Met Met Ser Gln His Ser Ala Gly Ala Arg Phe Arg Gln Ala Val Lys
1 5 10 15

Glu Ser Asn Pro Leu Ala Val Ala Gly Cys Val Asn Ala Tyr Phe Ala
20 25 30

Arg Leu Ala Thr Gln Ser Gly Phe Lys Ala Ile Tyr Leu Ser Gly Gly
35 40 45

Gly Val Ala Ala Cys Ser Cys Gly Ile Pro Asp Leu Gly Ile Thr Thr
50 55 60

Met Glu Asp Val Leu Ile Asp Ala Arg Arg Ile Thr Asp Asn Val Asp
65 70 75 80

Thr Pro Leu Leu Val Asp Ile Asp Val Gly Trp Gly Gly Ala Phe Asn
85 90 95

Ile Ala Arg Thr Ile Arg Asn Phe Glu Arg Ala Gly Val Ala Ala Val
100 105 110

His Ile Glu Asp Gln Val Ala Gln Lys Arg Cys Gly His Arg Pro Asn
115 120 125

Lys Ala Ile Val Ser Lys Asp Glu Met Val Asp Arg Ile Lys Ala Ala
130 135 140

Val Asp Ala Arg Val Asp Glu Asn Phe Val Ile Met Ala Arg Thr Asp
145 150 155 160

Ala Leu Ala Val Glu Gly Leu Asp Ala Ala Ile Glu Arg Ala Gln Ala
165 170 175

Cys Val Glu Ala Gly Ala Asp Met Ile Phe Pro Glu Ala Met Thr Asp
180 185 190

Leu Asn Met Tyr Arg Gln Phe Ala Asp Ala Val Lys Val Pro Val Leu
195 200 205

Ala Asn Ile Thr Glu Phe Gly Ser Thr Pro Leu Tyr Thr Gln Ser Glu
210 215 220

Leu Ala Glu Asn Gly Val Ser Leu Val Leu Tyr Pro Leu Ser Ser Phe
225 230 235 240

09030433 081601

Arg Ala Ala Ser Lys Ala Ala Leu Asn Val Tyr Glu Ala Ile Met Arg
245 250 255

Asp Gly Thr Ser Gly Gly Gly Gly Gly Gln Tyr Ala Asn Pro Cys Arg
260 265 270

Ala Val Arg Ala Ser Glu Leu Ser Cys Leu Arg Ala Lys Thr Gly
275 280 285

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<211> 921
<212> DNA
<213> Neisseria meningitidis

<220>
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<400> 37
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Met Pro Ser Ser Lys Asn Trp Ile Asn Cys Phe Lys Asn Asp Leu Pro
5 10 15
ctt tca gac tgc ctt tca aca aat ccg cat cgg tgg tct gaa aac ccg 96
Leu Ser Asp Cys Leu Ser Thr Asn Pro His Arg Ser Ser Glu Asn Pro
20 25 30
aaa ccc ata aaa aca caa agg aga aat acc atg acc gaa acc acc caa 144
Lys Pro Ile Lys Thr Gln Arg Arg Asn Thr Met Thr Glu Thr Thr Gln
35 40 45
acc cgg acc ctc aaa cct asa aaa tcc gtt cgg ctt tct ggc ggt gcg 192
Thr Pro Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala
50 55 60
gcc ggt aat acc ggt ttg tgt acc gtt ggc cgt acc ggc aac gat ttg 240
Ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu
65 70 75 80
agc tat cgc ggt tac gac att ctg gat ttg gca caa aaa tgt gag ttt 288
Ser Tyr Arg Gly Tyr Asp Ile Leu Asp Leu Ala Gln Lys Cys Glu Phe
85 90 95
gaa gaa gtt gcc cac ctg ctg att cac ggc cat tta ccc aac aaa ttc 336
Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe
100 105 110
gag ctg gcc gct tat aaa gcc aag ctt aaa tcc atg cgc ggc ctg cct 384
Glu Leu Ala Ala Tyr Lys Ala Lys Leu Lys Ser Met Arg Gly Leu Pro
115 120 125
atc cgt gtg att aaa gtt ttg gaa agc ctg cct gca cat acc cat ccg 432
Ile Arg Val Ile Lys Val Leu Glu Ser Leu Pro Ala His Thr His Pro
130 135 140
atg gac gtg atg cgt acc ggc gta tcc atg ctg ggc tgt gtt cat cct 480
Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro
145 150 155 160

004043 00460

gaa cgt gaa ggc cat ccg gaa agc gaa gcg cgc gac att gcc gac aaa	528
Glu Arg Glu Gly His Pro Glu Ser Glu Ala Arg Asp Ile Ala Asp Lys	
165 170 175	
ctg atc gcc agc ctc ggc agt atc ctc ttg tac tgg tat caa tat tcc	576
Leu Ile Ala Ser Leu Gly Ser Ile Leu Leu Tyr Trp Tyr Gln Tyr Ser	
180 185 190	
cac aac ggc aaa cgc att gaa gtt gaa agc gaa gaa gag acc atc ggc	624
His Asn Gly Lys Arg Ile Glu Val Glu Ser Glu Glu Thr Ile Gly	
195 200 205	
ggc cat ttc ctg cac ctg ttg cac ggc aaa cgc cca agc gaa tca cac	672
Gly His Phe Leu His Leu Leu His Gly Lys Arg Pro Ser Glu Ser His	
210 215 220	
atc aaa gcc atg cac gtt tca ctg att ctg tat gcc gaa cac gag ttc	720
Ile Lys Ala Met His Val Ser Leu Ile Leu Tyr Ala Glu His Glu Phe	
225 230 235 240	
aac gct tct acc ttt acc gcc cgc gtc atc gcc ggt aca ggc tct gat	768
Asn Ala Ser Thr Phe Thr Ala Arg Val Ile Ala Gly Thr Gly Ser Asp	
245 250 255	
atg tac tcc agc att acc gga gca atc gcc gcg ttg aaa ggt ccg aaa	816
Met Tyr Ser Ser Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Lys	
260 265 270	
cac gcc gcc gcc aac gaa ggg ctt acg ata ttc aaa aac gct acc gca	864
His Gly Gly Ala Asn Glu Gly Leu Thr Ile Phe Lys Asn Ala Thr Ala	
275 280 285	
atg ccg acg aag ccg aag ccg aca tcc gcc aac gca tcc gcc gca aag	912
Met Pro Thr Lys Pro Lys Pro Thr Ser Ala Asn Ala Ser Ala Ala Lys	
290 295 300	
aaa tcc tga	921
Lys Ser	
305	

<210> 38

<211> 306

<212> PRT

<213> Neisseria meningitidis

<400> 38

Met Pro Ser Ser Lys Asn Trp Ile Asn Cys Phe Lys Asn Asp Leu Pro	
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20 25 30	
Lys Pro Ile Lys Thr Gln Arg Arg Asn Thr Met Thr Glu Thr Thr Gln	
35 40 45	
Thr Pro Thr Leu Lys Pro Lys Lys Ser Val Ala Leu Ser Gly Val Ala	
50 55 60	

003043 001E0

Ala Gly Asn Thr Ala Leu Cys Thr Val Gly Arg Thr Gly Asn Asp Leu
65 70 75 80

Ser Tyr Arg Gly Tyr Asp Ile Leu Asp Leu Ala Gln Lys Cys Glu Phe
85 90 95

Glu Glu Val Ala His Leu Leu Ile His Gly His Leu Pro Asn Lys Phe
100 105 110

Glu Leu Ala Ala Tyr Lys Ala Lys Leu Lys Ser Met Arg Gly Leu Pro
115 120 125

Ile Arg Val Ile Lys Val Leu Glu Ser Leu Pro Ala His Thr His Pro
130 135 140

Met Asp Val Met Arg Thr Gly Val Ser Met Leu Gly Cys Val His Pro
145 150 155 160

Glu Arg Glu Gly His Pro Glu Ser Glu Ala Arg Asp Ile Ala Asp Lys
165 170 175

Leu Ile Ala Ser Leu Gly Ser Ile Leu Leu Tyr Trp Tyr Gln Tyr Ser
180 185 190

His Asn Gly Lys Arg Ile Glu Val Glu Ser Glu Glu Glu Thr Ile Gly
195 200 205

Gly His Phe Leu His Leu Leu His Gly Lys Arg Pro Ser Glu Ser His
210 215 220

Ile Lys Ala Met His Val Ser Leu Ile Leu Tyr Ala Glu His Glu Phe
225 230 235 240

Asn Ala Ser Thr Phe Thr Ala Arg Val Ile Ala Gly Thr Gly Ser Asp
245 250 255

Met Tyr Ser Ser Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Lys
260 265 270

His Gly Gly Ala Asn Glu Gly Leu Thr Ile Phe Lys Asn Ala Thr Ala
275 280 285

Met Pro Thr Lys Pro Lys Pro Thr Ser Ala Asn Ala Ser Ala Ala Lys
290 295 300

Lys Ser
305

<210> 39
<211> 945
<212> DNA
<213> Neisseria meningitidis

<220>
<221> CDS
<222> (1)..(942)

09830433.DAT

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Met His Leu Cys Gly Lys Tyr Tyr Gly Val Asn Met Lys Leu Arg Asp	
1 5 10 15	
tta ctg atg gga ata ttc ttg gca gtt tct gcg gcc ctt ctg aat gca	96
Leu Leu Met Gly Ile Phe Leu Ala Val Ser Ala Ala Leu Leu Asn Ala	
20 25 30	
acc atc ggc ata ttc agc aag ata ttg atg gag cag ggc ttg tct gtt	144
Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val	
35 40 45	
cag cat att gca ttt ttg aaa act ttg aca ggt ttc gtg ttt atc agc	192
Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser	
50 55 60	
att ttg ctt tgc cgt acc ggt ttt acc aga cag att gcg gat att tca	240
Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser	
65 70 75 80	
aga aag aaa gag gca att ttg ccg ttg ctg tta aaa gta gca att tgt	288
Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Leu Lys Val Ala Ile Cys	
85 90 95	
gct ttt ttc gga att tat acg ttg ttt ttc ttt gaa acc aca gct tat	336
Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr	
100 105 110	
caa tat ggc aat gct gcg aat gta gta gtt gta tta atg gca tcg gct	384
Gln Tyr Gly Asn Ala Ala Asn Val Val Val Leu Met Ala Ser Ala	
115 120 125	
gcc gta tct gcc ttg ata ttg gac agc ata ctg tta gat gaa cgt att	432
Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile	
130 135 140	
tgc att tct tca gtc gtc ggt gtg ggt ttg gca gta ttg ggg atc gca	480
Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala	
145 150 155 160	
atg att tct tgg act gga gaa gga agt tta ggg ttg att ctg aat gcc	528
Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala	
165 170 175	
gca ctg gcg ggc tcg gcc tac ggt tgt ttt tcc gtt ttg att aag aaa	576
Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys	
180 185 190	
ttc ggc cta aac ggc ggt att tat ttg aca cgg ata ttg atg ttt ttt	624
Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe	
195 200 205	
gga agt att ttt ttg ttt atc cct tca ttg gaa ggt att gag gat ata	672
Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile	
210 215 220	
cat tgg caa tgg tct ttt att ccg cca ctc ttg gca ttg tct tta ttg	720
His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu	
225 230 235 240	

09030433 081604

ccg acg att tta gga ttt tat tgt aca act aaa gca ttg gat tat ttg	768
Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu	
245 250 255	
agt gct gcg aag gta cag gta act gaa ttg gcc gag cca ttg ttt gct	816
Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala	
260 265 270	
gcc gta ctg gct tgg ttg ttt ttg aat gaa ata ccg gaa gga cgc ttc	864
Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe	
275 280 285	
ttt gtc gcc gcc att ctg att att gcc ggt att gtg tct atc aat ggg	912
Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly	
290 295 300	
ctg tat cga cca ttg ttg aag cga att gaa taa	945
Leu Tyr Arg Pro Leu Leu Lys Arg Ile Glu	
305 310	

<210> 40
 <211> 314
 <212> PRT
 <213> Neisseria meningitidis

<400> 40

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Thr Ile Gly Ile Phe Ser Lys Ile Leu Met Glu Gln Gly Leu Ser Val	
35 40 45	
Gln His Ile Ala Phe Leu Lys Thr Leu Thr Gly Phe Val Phe Ile Ser	
50 55 60	
Ile Leu Leu Cys Arg Thr Gly Phe Thr Arg Gln Ile Ala Asp Ile Ser	
65 70 75 80	
Arg Lys Lys Glu Ala Ile Leu Pro Leu Leu Leu Lys Val Ala Ile Cys	
85 90 95	
Ala Phe Phe Gly Ile Tyr Thr Leu Phe Phe Phe Glu Thr Thr Ala Tyr	
100 105 110	
Gln Tyr Gly Asn Ala Ala Asn Val Val Val Val Leu Met Ala Ser Ala	
115 120 125	
Ala Val Ser Ala Leu Ile Leu Asp Ser Ile Leu Leu Asp Glu Arg Ile	
130 135 140	
Cys Ile Ser Ser Val Val Gly Val Gly Leu Ala Val Leu Gly Ile Ala	
145 150 155 160	
Met Ile Ser Trp Thr Gly Glu Gly Ser Leu Gly Leu Ile Leu Asn Ala	
165 170 175	

0983043 08150

Ala Leu Ala Gly Ser Gly Tyr Gly Cys Phe Ser Val Leu Ile Lys Lys
 180 185 190

Phe Gly Leu Asn Gly Gly Ile Tyr Leu Thr Arg Ile Leu Met Phe Phe
 195 200 205

Gly Ser Ile Phe Leu Phe Ile Pro Ser Leu Glu Gly Ile Glu Asp Ile
 210 215 220

His Trp Gln Trp Ser Phe Ile Pro Pro Leu Leu Ala Leu Ser Leu Leu
 225 230 235 240

Pro Thr Ile Leu Gly Phe Tyr Cys Thr Thr Lys Ala Leu Asp Tyr Leu
 245 250 255

Ser Ala Ala Lys Val Gln Val Thr Glu Leu Ala Glu Pro Leu Phe Ala
 260 265 270

Ala Val Leu Ala Trp Leu Phe Leu Asn Glu Ile Pro Glu Gly Arg Phe
 275 280 285

Phe Val Gly Ala Ile Leu Ile Ile Ala Gly Ile Val Ser Ile Asn Gly
 290 295 300

Leu Tyr Arg Pro Leu Leu Lys Arg Ile Glu
 305 310

<210> 41
 <211> 2610
 <212> DNA
 <213> Neisseria meningitidis

<220>
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 <222> (1)..(2607)

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 Met Ala Ala Asn Gln Arg Tyr Arg Lys Pro Leu Pro Gly Thr Asp Leu
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gaa tac tac gac gcg cgt gcg gcg tgt gag gac atc aag ccc ggc tct 96
 Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Asp Ile Lys Pro Gly Ser
 20 25 30

tac gac aag ctg cct tac acg agc cgc att ttg gcg gag aat ttg gtc 144
 Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
 35 40 45

aac cgc gcg gac aaa gtc gat ttg ccg acg ctg caa agc tgg ctg ggt 192
 Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
 50 55 60

cag ctg att gag gga aaa cag gaa atc gac ttt cct tgg tat ccg gcg 240
 Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
 65 70 75 80

cgg gtg gtg tgc cac gat att ctg ggg cag acc gcg ttg gtg gat ttg 288

093043-08160

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu	85	90	95	
gca ggt ctg cgc gat gcg att gcc gaa aaa ggc ggc gat cct gcc aaa	336			
Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys	100	105	110	
gtg aat ccg gtg gtt gca aaa ccc agc ttc atc gtc gac cac tct ctg	384			
Val Asn Pro Val Val Ala Lys Pro Ser Phe Ile Val Asp His Ser Leu	115	120	125	
gcc gtt gaa tgc ggc ggc tac gac ccc gat gcc ttc cgc aaa aac cgc	432			
Ala Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg	130	135	140	
caa atc gaa gac aga cgt aac gaa gac cgt ttc cac ttc atc aac tgg	480			
Gln Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp	145	150	155	160
aca aaa acc gca ttt gaa aat gtg gac gtg att ccg gcg ggc aac ggc	528			
Thr Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly	165	170	175	
atc atg cac caa atc aat cta gaa aaa atg tgc ccc gtc gtc caa gtc	576			
Ile Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val	180	185	190	
aaa aac ggc gtg gcg ttc ccc gat acc tgc gtc ggc acg gat tgc cac	624			
Lys Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His	195	200	205	
acg ccg cac gtc gat gcg ctg ggc gtg att tcc gtg ggc gtg ggc gga	672			
Thr Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly	210	215	220	
ttg gaa gcg gaa acc gtg atg ctg ggt cgc gcg tcc atg atg cgc ctg	720			
Leu Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu	225	230	235	240
ccc gat att gtc ggc gtt gag ctg aac ggc aaa ccg cag gcg ggc att	768			
Pro Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Gln Ala Gly Ile	245	250	255	
acg gcg acg gat att gtg ttg gca ctg acc gag ttt ctg cgc aaa gaa	816			
Thr Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu	260	265	270	
cgc gtg gtc ggg gcg ttt gtc gaa ttc ttc ggc gag ggc gcg aga agc	864			
Arg Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser	275	280	285	
ctg tct atc ggc gac cgc gcg acc att tcc aac atg acg ccg gag ttc	912			
Leu Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe	290	295	300	
ggc gcg act gcc gcg atg ttc gct att gat gag caa acc att gat tat	960			
Gly Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr	305	310	315	320
ttg aaa ctg acc gga cgc gac gac gcg cag gtg aaa ttg gtg gaa acc	1008			

09630433-081601

Leu	Lys	Leu	Thr	Gly 325	Arg	Asp	Asp	Ala	Gln 330	Val	Lys	Leu	Val	Glu 335	Thr	
tac	gcc	aaa	acc	gca	ggc	tta	tgg	gca	gat	gcc	ttg	aaa	acc	gcc	gtc	1056
Tyr	Ala	Lys	Thr	Ala	Gly	Leu	Trp	Ala	Asp	Ala	Leu	Lys	Thr	Ala	Val	
			340					345					350			
tat	ccg	cgc	gtt	ttg	aaa	ttt	gat	ttg	agc	agc	gta	acg	cgc	aat	atg	1104
Tyr	Pro	Arg	Val	Leu	Lys	Phe	Asp	Leu	Ser	Ser	Val	Thr	Arg	Asn	Met	
			355				360					365				
gca	ggc	ccg	agc	aac	ccg	cac	gcg	cgt	ttt	gcg	acc	gcc	gat	ttg	gcc	1152
Ala	Gly	Pro	Ser	Asn	Pro	His	Ala	Arg	Phe	Ala	Thr	Ala	Asp	Leu	Ala	
			370			375					380					
agc	aaa	ggc	ttg	gct	aaa	cct	tac	gaa	gag	cct	tca	gac	ggc	caa	atg	1200
Ser	Lys	Gly	Leu	Ala	Lys	Pro	Tyr	Glu	Glu	Pro	Ser	Asp	Gly	Gln	Met	
					390					395					400	
ccc	gac	ggc	gcg	gtc	atc	atc	gcc	gcg	att	acc	agt	tgc	acc	aac	act	1248
Pro	Asp	Gly	Ala	Val	Ile	Ile	Ala	Ala	ile	Thr	Ser	Cys	Thr	Asn	Thr	
				405					410					415		
tcc	aac	ccg	cgc	aac	gtt	gtt	gcc	gcc	gcg	ctc	ttg	gcg	cgc	aac	gcc	1296
Ser	Asn	Pro	Arg	Asn	Val	Val	Ala	Ala	Ala	Leu	Leu	Ala	Arg	Asn	Ala	
			420					425					430			
aac	tgc	ttc	ggg	ctg	aaa	cgc	aaa	ccg	tgg	gtc	aaa	acc	tgc	ttt	gcc	1344
Asn	Cys	Phe	Gly	Leu	Lys	Arg	Lys	Pro	Trp	Val	Lys	Thr	Ser	Phe	Ala	
			435				440					445				
ccc	ggt	tgc	aaa	gtg	gcg	gaa	att	tat	ttg	aaa	gaa	gca	ggc	ctg	ctg	1392
Pro	Gly	Ser	Lys	Val	Ala	Glu	Ile	Tyr	Leu	Lys	Glu	Ala	Gly	Leu	Leu	
			450			455					460					
ccc	gaa	atg	gaa	aaa	ctc	ttc	ggt	atc	gtc	gcc	ttc	gcc	tgc	acc		1440
Pro	Glu	Met	Glu	Lys	Leu	Gly	Phe	Gly	Ile	Val	Ala	Phe	Ala	Cys	Thr	
			465		470				475					480		
acc	tgc	aac	ggc	atg	agt	ggc	gcg	ctg	gat	ccg	aaa	atc	cag	aaa	gaa	1488
Thr	Cys	Asn	Gly	Met	Ser	Gly	Ala	Leu	Asp	Pro	Lys	Ile	Gln	Lys	Glu	
				485					490				495			
atc	atc	gac	cgc	gat	ttg	tac	gcc	acc	gcc	gta	tta	tca	ggc	aac	cgc	1536
Ile	Ile	Asp	Arg	Asp	Leu	Tyr	Ala	Thr	Ala	Val	Leu	Ser	Gly	Asn	Arg	
			500					505					510			
aac	ttc	gac	ggc	cgt	gtc	cat	ccg	tat	gcg	aaa	cag	gct	ttc	ctc	gct	1584
Asn	Phe	Asp	Gly	Arg	Val	His	Pro	Tyr	Ala	Lys	Gln	Ala	Phe	Leu	Ala	
			515				520					525				
tcg	cct	ccg	ttg	gtc	gtt	gcc	tac	gcg	ctg	gca	ggc	agt	atc	cgt	ttc	1632
Ser	Pro	Pro	Leu	Val	Val	Ala	Tyr	Ala	Leu	Ala	Gly	Ser	Ile	Arg	Phe	

Leu Lys Asp Ile Trp Pro Ala Asp Glu Glu Ile Asp Ala Val Val Ala	
565 570 575	
gaa tat gtg aaa ccg cag cag ttc cgc gat gtg tat gta ccg atg ttc	1776
Glu Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Val Pro Met Phe	
580 585 590	
gac acc ggc aca gcg caa aaa gca cct agt ccg ctg tac gat tgg cgt	1824
Asp Thr Gly Thr Ala Gln Lys Ala Pro Ser Pro Leu Tyr Asp Trp Arg	
595 600 605	
ccg atg tcc acc tac atc cgc cgt ccg cct tac tgg gaa ggc gcg ctg	1872
Pro Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu	
610 615 620	
gca ggg gaa cgc aca tta aga ggt atg cgt ccg ctg gcg att ttg ccc	1920
Ala Gly Glu Arg Thr Leu Arg Gly Met Arg Pro Leu Ala Ile Leu Pro	
625 630 635 640	
gac aac atc acc acc gac cac ctg tgc ccg tcc aat gcg att ttg gcc	1968
Asp Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala	
645 650 655	
gtc agt gcc gca ggc gag tat ttg gcg aaa atg ggt ttg cct gaa gaa	2016
Val Ser Ala Ala Gly Glu Tyr Leu Ala Lys Met Gly Leu Pro Glu Glu	
660 665 670	
gac ttc aac tct tac gca acc cac cgc ggc gac cac ttg acc gcc caa	2064
Asp Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln	
675 680 685	
cgc gct acc ttc gcc aat ccg aaa ctg ttt aac gaa atg gtg aaa aac	2112
Arg Ala Thr Phe Ala Asn Pro Lys Leu Phe Asn Glu Met Val Lys Asn	
690 695 700	
gaa gac ggc agc gtg cgc caa ggc tgc ttc gcc cgc gtc gaa ccc gaa	2160
Glu Asp Gly Ser Val Arg Gln Gly Ser Phe Ala Arg Val Glu Pro Glu	
705 710 715 720	
ggc gaa acc atg cgc atg tgg gaa gcc atc gaa acc tat atg aac cgc	2208
Gly Glu Thr Met Arg Met Trp Glu Ala Ile Glu Thr Tyr Met Asn Arg	
725 730 735	
aaa cag ccg ctg atc atc att gcc ggt gcg gac tat ggt caa ggc tca	2256
Lys Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser	
740 745 750	
agc cgc gac tgg gct gca aaa ggc gta cgc ctg gcc ggc gta gaa gcg	2304
Ser Arg Asp Trp Ala Ala Lys Gly Val Arg Leu Ala Gly Val Glu Ala	
755 760 765	
att gtt gcc gaa ggc ttc gag cgt atc cac cgc acc aac ctt atc ggc	2352
Ile Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly	
770 775 780	
atg ggc gtg ttg ccg ctg cag ttc aaa ccc gac acc aac cgc cat acc	2400
Met Gly Val Leu Pro Leu Gln Phe Lys Pro Asp Thr Asn Arg His Thr	
785 790 795 800	
ctg caa ctg gac ggt acg gaa acc tac gac gtg gtc ggc gaa cgc aca	2448

093043 093043

Leu Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr
805 810 815

cgc cgc tgc gac ctg acc ctc gtg att cac cgt aaa aac ggc gaa acc 2496
Pro Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr
820 825 830

gtc gaa gtt ccc gtt acc tgc cgc ctc gat act gca gaa gaa gta ttg 2544
Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu
835 840 845

gta tat gaa gcc ggc ggc gtg ttg caa cgg ttt gca cag gat ttt ttg 2592
Val Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu
850 855 860

gaa ggg aac gcg gct tag 2610
Glu Gly Asn Ala Ala
865

<210> 42
<211> 869
<212> PRT
<213> Neisseria meningitidis

<400> 42
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Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Asp Ile Lys Pro Gly Ser
20 25 30

Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
35 40 45

Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
50 55 60

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
65 70 75 80

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu
85 90 95

Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys
100 105 110

Val Asn Pro Val Val Ala Lys Pro Ser Phe Ile Val Asp His Ser Leu
115 120 125

Ala Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg
130 135 140

Gln Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp
145 150 155 160

Thr Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly
165 170 175

Ile Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val

009180"EE40E360

180	185	190
Lys Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His		
195	200	205
Thr Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly		
210	215	220
Leu Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu		
225	230	235
Pro Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Gln Ala Gly Ile		
245	250	255
Thr Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu		
260	265	270
Arg Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser		
275	280	285
Leu Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe		
290	295	300
Gly Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr		
305	310	315
Leu Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr		
325	330	335
Tyr Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val		
340	345	350
Tyr Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met		
355	360	365
Ala Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala		
370	375	380
Ser Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met		
385	390	395
Pro Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr		
405	410	415
Ser Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala		
420	425	430
Asn Cys Phe Gly Leu Lys Arg Lys Pro Trp Val Lys Thr Ser Phe Ala		
435	440	445
Pro Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Gly Leu Leu		
450	455	460
Pro Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr		
465	470	475
Thr Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu		
485	490	495
Ile Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg		

09030433 081501

500					505					510					
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		515					520					525			
Ser	Pro	Pro	Leu	Val	Val	Ala	Tyr	Ala	Leu	Ala	Gly	Ser	Ile	Arg	Phe
		530				535					540				
Asp	Ile	Glu	Asn	Asp	Val	Leu	Gly	Val	Ala	Asp	Gly	Lys	Glu	Ile	Arg
					550					555					560
Leu	Lys	Asp	Ile	Trp	Pro	Ala	Asp	Glu	Glu	Ile	Asp	Ala	Val	Val	Ala
				565					570					575	
Glu	Tyr	Val	Lys	Pro	Gln	Gln	Phe	Arg	Asp	Val	Tyr	Val	Pro	Met	Phe
			580					585					590		
Asp	Thr	Gly	Thr	Ala	Gln	Lys	Ala	Pro	Ser	Pro	Leu	Tyr	Asp	Trp	Arg
		595					600					605			
Pro	Met	Ser	Thr	Tyr	Ile	Arg	Arg	Pro	Pro	Tyr	Trp	Glu	Gly	Ala	Leu
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Ala	Gly	Glu	Arg	Thr	Leu	Arg	Gly	Met	Arg	Pro	Leu	Ala	Ile	Leu	Pro
					630					635					640
Asp	Asn	Ile	Thr	Thr	Asp	His	Leu	Ser	Pro	Ser	Asn	Ala	Ile	Leu	Ala
				645					650					655	
Val	Ser	Ala	Ala	Gly	Glu	Tyr	Leu	Ala	Lys	Met	Gly	Leu	Pro	Glu	Glu
			660					665					670		
Asp	Phe	Asn	Ser	Tyr	Ala	Thr	His	Arg	Gly	Asp	His	Leu	Thr	Ala	Gln
		675					680					685			
Arg	Ala	Thr	Phe	Ala	Asn	Pro	Lys	Leu	Phe	Asn	Glu	Met	Val	Lys	Asn
		690				695					700				
Glu	Asp	Gly	Ser	Val	Arg	Gln	Gly	Ser	Phe	Ala	Arg	Val	Glu	Pro	Glu
					710					715					720
Gly	Glu	Thr	Met	Arg	Met	Trp	Glu	Ala	Ile	Glu	Thr	Tyr	Met	Asn	Arg
				725					730					735	
Lys	Gln	Pro	Leu	Ile	Ile	Ile	Ala	Gly	Ala	Asp	Tyr	Gly	Gln	Gly	Ser
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Ser	Arg	Asp	Trp	Ala	Ala	Lys	Gly	Val	Arg	Leu	Ala	Gly	Val	Glu	Ala
		755					760					765			
Ile	Val	Ala	Glu	Gly	Phe	Glu	Arg	Ile	His	Arg	Thr	Asn	Leu	Ile	Gly
		770				775					780				
Met	Gly	Val	Leu	Pro	Leu	Gln	Phe	Lys	Pro	Asp	Thr	Asn	Arg	His	Thr
					790					795					800
Leu	Gln	Leu	Asp	Gly	Thr	Glu	Thr	Tyr	Asp	Val	Val	Gly	Glu	Arg	Thr
				805					810					815	
Pro	Arg	Cys	Asp	Leu	Thr	Leu	Val	Ile	His	Arg	Lys	Asn	Gly	Glu	Thr

820 825 830
Val Glu Val Pro Val Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu
835 840 845
Val Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu
850 855 860
Glu Gly Asn Ala Ala
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<213> Neisseria meningitidis

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Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu
20 25 30
gcg gga agc gca cgc gac aaa atc ctc ttg cgc gta ctc ggc agc ccg 144
Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
35 40 45
gac ccc tac ggc aag cag ata gac ggt ttg ggc aac gcc agt tcg tcc 192
Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
50 55 60
acc agc aaa gcc gtg att ttg gac aag tcc gaa cgc acc gat cac gat 240
Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp
65 70 75 80
gtc gat tac ctt ttc ggg caa gtt tcc atc gac aaa cct ttt gtc gat 288
Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
85 90 95
tgg agt ggc aac tgc ggc aac ctc acc gcc gcc gtg ggc gca ttt gcc 336
Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
100 105 110
atc gag caa ggc ttg gtc gat aaa tcc aaa atc cct tca gac ggc ccg 384
Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro
115 120 125
tgt acc gtc aaa atc tgg cag aaa aac atc ggc aaa acc att att gcc 432
Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala
130 135 140
cat gta ccg atg caa aac ggc gca gtt ttg gaa aca ggc gat ttt gag 480

000043.081504

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu	
145 150 155 160	
ctc gac ggc gta acg ttc ccg gca gcc gaa gta caa atc gaa ttt ctt	528
Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu	
165 170 175	
gat cca gcc gac ggc gaa ggc agt atg ttc cca acc ggc aat ttg gtc	576
Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val	
180 185 190	
gat gaa att gat gtg ccg aat ata ggc cgt ttg aaa gcc acg ctc atc	624
Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile	
195 200 205	
aac gcg ggc att ccg acc gtt ttc ctg aat gcc gcc gac ttg ggc tac	672
Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr	
210 215 220	
acg ggc aaa gag ttg caa gac gac atc aac aac gat gcc gca gct ttg	720
Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu	
225 230 235 240	
gaa aaa ttc gag aaa atc cgc gct tac ggt gcg ctg aaa atg ggt cta	768
Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu	
245 250 255	
atc agc gac gta tcc gaa gct gcc gcc cgc gcg cac acg ccg aaa gtc	816
Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val	
260 265 270	
gcc ttc gtc gcg ccc gcc gcc gat tac acc gcc tcc agt ggc aaa acc	864
Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr	
275 280 285	
gtg aat gcc gcc gac atc gat ttg ctg gta cgc gcc ctg agc atg ggc	912
Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly	
290 295 300	
aaa ttg cac cac gcg atg atg ggt acc gcc tct gtt gcc att gcg acc	960
Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr	
305 310 315 320	
gcc gcc gcc gtg ccc ggt acg ctg gtc aac ctt gcc gca ggg gcg gga	1008
Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Ala Gly	
325 330 335	
acg cgt aaa gaa gtg cgc ttc ggg cat cct tcc ggc aca ttg cgc gtc	1056
Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val	
340 345 350	
ggt gca gcc gcc gaa tgt cag gac gga caa tgg acg gcc acc aaa gcg	1104
Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala	
355 360 365	
gtt atg agc cgc agc gca cgc gtg atg atg gaa ggt tgg gtc agg gtg	1152
Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val	
370 375 380	
ccg gaa gat tgt ttt taa	1170
Pro Glu Asp Cys Phe	
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<211> 389

<212> PRT

093043 091601

<213> Neisseria meningitidis

<400> 44

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Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
      35              40              45

Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
      50              55              60

Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Thr Asp His Asp
      65              70              75              80

Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
      85              90              95

Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
      100             105             110

Ile Glu Gln Gly Leu Val Asp Lys Ser Lys Ile Pro Ser Asp Gly Pro
      115             120             125

Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala
      130             135             140

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu
      145             150             155             160

Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu
      165             170             175

Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val
      180             185             190

Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile
      195             200             205

Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr
      210             215             220

Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu
      225             230             235             240

Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu
      245             250             255

Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val
      260             265             270

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093043-081604

Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr
 275 280 285

Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly
 290 295 300

Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr
 305 310 315 320

Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Ala Gly
 325 330 335

Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
 340 345 350

Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala
 355 360 365

Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val
 370 375 380

Pro Glu Asp Cys Phe
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 Ala Met Leu Pro Ala Cys Trp Ala Gln Ala Met Leu Ala Glu Val Ile
 20 25 30

agc tgc aac aag gct tcc tcc ctg ccg cag cct tcc gcg aga tcc gcg 144
 Ser Cys Asn Lys Ala Ser Ser Leu Pro Gln Pro Ser Ala Arg Ser Ala
 35 40 45

ttt aaa tca acc tgc ttc atg ggt gat tct ccg tat ttg gtt cag ata 192
 Phe Lys Ser Thr Cys Phe Met Gly Asp Ser Pro Tyr Leu Val Gln Ile
 50 55 60

gac ttg gtt ttt gcg ccg cag gcc ggt gcc ttc ttt caa gcc gat tat 240
 Asp Leu Val Phe Ala Pro Gln Gly Gly Gly Phe Phe Gln Ala Asp Tyr
 65 70 75 80

ttt gaa ttt gac ttt gct gcc gaa gcg cac ctg tgc cag cct gcc caa 288
 Phe Glu Phe Asp Phe Ala Ala Glu Ala His Leu Cys Gln Pro Ala Gln
 85 90 95

009499-0340360

atc ggc ggc ggc aac ggt agc gat ttt cgg ata acc gcc ggt ggt ttg	336
Ile Gly Gly Gly Asn Gly Ser Asp Phe Arg Ile Thr Ala Gly Gly Leu	
100 105 110	
cgc atc ggc cag cag gat aat cgg ttt gcc gcc ggg cgg cac ctg cac	384
Arg Ile Gly Gln Gln Asp Asn Arg Phe Ala Ala Gly Arg His Leu His	
115 120 125	
ggt tcc tgc ctg aac agc gtg gga cag cat ttc caa agg ttg cga cag	432
Gly Ser Cys Leu Asn Ser Val Gly Gln His Phe Gln Arg Leu Arg Gln	
130 135 140	
ggt cag cgg ctg tcc gtc gaa gcg gta gcc cat gcg gtt gct atc gct	480
Gly Gln Arg Leu Ser Val Glu Ala Val Ala His Ala Val Ala Ile Ala	
145 150 155 160	
ttg cag cgt cca cgt ttc ccg ttc cag att cag acg ccc ttt ttc act	528
Leu Gln Arg Pro Arg Phe Pro Phe Gln Ile Gln Thr Pro Phe Phe Thr	
165 170 175	
gaa agc ggc ata ttc cga cga agg aac aag gtg gat ggt atc ggt aaa	576
Glu Ser Gly Ile Phe Arg Arg Arg Asn Lys Val Asp Gly Ile Gly Lys	
180 185 190	
cgg tat cgg ggc aat gcc gac ttt gga caa ttc ctg cgc acc ttt gcc	624
Arg Tyr Arg Gly Asn Ala Asp Phe Gly Gln Phe Leu Arg Trp Phe Ala	
195 200 205	
gat ggg gag ata atc gcc ttt tgg cag cat tcc gcc ctg atg gcc gcc	672
Asp Gly Glu Ile Ile Ala Phe Leu Gln His Ser Ala Leu Met Ala Ala	
210 215 220	
gaa atc ggc ttt cag gtc ggt gct tcc cga acc cat cac ttc cgg cac	720
Glu Thr Gly Phe Gln Val Gly Ala Ser Arg Thr His His Phe Arg His	
225 230 235 240	
atc aaa tcc gcc cgc cac gca cac ata gcc gta cat gcc ctg cac ggc	768
Ile Lys Ser Ala Arg His Ala His Ile Ala Val His Ala Leu His Gly	
245 250 255	
acg cac cat ttt caa ggt ctg ccc ttt gcg gcc ggt ata acg cca ata	816
Thr His His Phe Gln Gly Leu Pro Phe Ala Gly Gly Ile Thr Pro Ile	
260 265 270	
cga ata gac cgg ttc gcc gtc caa ttc cgc ctg ata cac gcc acc ggt	864
Arg Ile Asp Arg Phe Ala Val Gln Phe Arg Leu Ile His Gly Thr Gly	
275 280 285	
gag aca aaa cgg cgt atc ccg ttc aaa cac cag cat tat ccc gcc caa	912
Glu Thr Lys Arg Arg Ile Pro Phe Lys His Gln His Tyr Pro Ala Gln	
290 295 300	
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Ser Asp Phe Asp Cys Gly Arg Ala Phe Val Val Ala Gln	
305 310 315	

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 <213> Neisseria meningitidis

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<400> 46

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			20				25						30		
Ser	Cys	Asn	Lys	Ala	Ser	Ser	Leu	Pro	Gln	Pro	Ser	Ala	Arg	Ser	Ala
		35					40					45			
Phe	Lys	Ser	Thr	Cys	Phe	Met	Gly	Asp	Ser	Pro	Tyr	Leu	Val	Gln	Ile
	50					55					60				
Asp	Leu	Val	Phe	Ala	Pro	Gln	Gly	Gly	Gly	Phe	Phe	Gln	Ala	Asp	Tyr
	65				70					75					80
Phe	Glu	Phe	Asp	Phe	Ala	Ala	Glu	Ala	His	Leu	Cys	Gln	Pro	Ala	Gln
				85					90					95	
Ile	Gly	Gly	Gly	Asn	Gly	Ser	Asp	Phe	Arg	Ile	Thr	Ala	Gly	Gly	Leu
			100					105						110	
Arg	Ile	Gly	Gln	Gln	Asp	Asn	Arg	Phe	Ala	Ala	Gly	Arg	His	Leu	His
		115					120						125		
Gly	Ser	Cys	Leu	Asn	Ser	Val	Gly	Gln	His	Phe	Gln	Arg	Leu	Arg	Gln
		130				135						140			
Gly	Gln	Arg	Leu	Ser	Val	Gln	Ala	Val	Ala	His	Ala	Val	Ala	Ile	Ala
	145				150					155					160
Leu	Gln	Arg	Pro	Arg	Phe	Pro	Phe	Gln	Ile	Gln	Thr	Pro	Phe	Phe	Thr
				165					170						175
Glu	Ser	Gly	Ile	Phe	Arg	Arg	Arg	Asn	Lys	Val	Asp	Gly	Ile	Gly	Lys
			180					185					190		
Arg	Tyr	Arg	Gly	Asn	Ala	Asp	Phe	Gly	Gln	Phe	Leu	Arg	Thr	Phe	Ala
		195				200							205		
Asp	Gly	Glu	Ile	Ile	Ala	Phe	Leu	Gln	His	Ser	Ala	Leu	Met	Ala	Ala
	210					215					220				
Glu	Thr	Gly	Phe	Gln	Val	Gly	Ala	Ser	Arg	Thr	His	His	Phe	Arg	His
	225				230					235					240
Ile	Lys	Ser	Ala	Arg	His	Ala	His	Ile	Ala	Val	His	Ala	Leu	His	Gly
			245					250						255	
Thr	His	His	Phe	Gln	Gly	Leu	Pro	Phe	Ala	Gly	Gly	Ile	Thr	Pro	Ile
			260					265					270		
Arg	Ile	Asp	Arg	Phe	Ala	Val	Gln	Phe	Arg	Leu	Ile	His	Gly	Thr	Gly
		275					280						285		
Glu	Thr	Lys	Arg	Arg	Ile	Pro	Phe	Lys	His	Gln	His	Tyr	Pro	Ala	Gln
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ctg aat gcg cct tcc gaa ctg ggc aaa cag caa aag ttg tgg gcg ttt																96
Leu	Asn	Ala	Pro	Ser	Glu	Leu	Gly	Lys	Gln	Gln	Lys	Leu	Trp	Ala	Phe	
			20					25					30			
gcc gct gcg ctc ggg cag cac gac agg att gag gaa gtg gtg gtc ggc																144
Ala	Ala	Ala	Leu	Gly	Gln	His	Asp	Arg	Ile	Glu	Glu	Val	Val	Val	Gly	
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atg aac aat ctg acc gtg ttc acc cgt ttc gat acc gat ttg gcg acg																192
Met	Asn	Asn	Leu	Thr	Val	Phe	Thr	Arg	Phe	Asp	Thr	Asp	Leu	Ala	Thr	
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ctt gcc gat gaa ttg caa tat gtg tgg gaa cac acc gcc gtt aca gac																240
Leu	Ala	Asp	Glu	Leu	Gln	Tyr	Val	Trp	Glu	His	Thr	Ala	Val	Thr	Asp	
65					70					75					80	
cat cag gcc aaa ctg gtg gaa att ccc gtc tgc tac gcc gcc gaa tac																288
His	Gln	Gly	Lys	Leu	Val	Glu	Ile	Pro	Val	Cys	Tyr	Gly	Gly	Glu	Tyr	
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ggc ccg gat ttg gcg gaa gtc gct gct ttc cat cag acg gtt att tcc																336
Gly	Pro	Asp	Leu	Ala	Glu	Val	Ala	Ala	Phe	His	Gln	Thr	Val	Ile	Ser	
			100					105					110			
gaa atc gtc cgc cgc cat acg gcg caa att tat acc gta ttt atg atg																384
Glu	Ile	Val	Arg	Arg	His	Thr	Ala	Gln	Thr	Tyr	Thr	Val	Phe	Met	Met	
			115				120					125				
ggc ttc cag cct ggt ttc cct tat ctg gcc gcc ttg ccc gaa gca ttg																432
Gly	Phe	Gln	Pro	Gly	Phe	Pro	Tyr	Leu	Gly	Gly	Leu	Pro	Glu	Ala	Leu	
	130					135					140					
cac acg ccc cgc cgt gcc gtg ccg aga acg tcc gtt cct gcc ggt tgg																480
His	Thr	Pro	Arg	Arg	Ala	Val	Pro	Arg	Thr	Ser	Val	Pro	Ala	Gly	Ser	
145					150					155					160	
gtc ggt atc gcc gcc agt cag acc ggt gtg tat ccg ttc gct tgc ccc																528
Val	Gly	Ile	Gly	Gly	Ser	Gln	Thr	Gly	Val	Tyr	Pro	Phe	Ala	Ser	Pro	
				165					170					175		

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 Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala
 180 185 190

gat ttg aat ccg ccg acc ctg ctg gcg gcg ggt gac caa gtc cgc ttt 624
 Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe
 195 200 205

gtt gca gaa agg att gag cca tga 648
 Val Ala Glu Arg Ile Glu Pro
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 35 40 45

Met Asn Asn Leu Thr Val Phe Thr Arg Phe Asp Thr Asp Leu Ala Thr
 50 55 60

Leu Ala Asp Glu Leu Gln Tyr Val Trp Glu His Thr Ala Val Thr Asp
 65 70 75 80

His Gln Gly Lys Leu Val Gln Ile Pro Val Cys Tyr Gly Gly Glu Tyr
 85 90 95

Gly Pro Asp Leu Ala Glu Val Ala Ala Phe His Gln Thr Val Ile Ser
 100 105 110

Glu Ile Val Arg Arg His Thr Ala Gln Thr Tyr Thr Val Phe Met Met
 115 120 125

Gly Phe Gln Pro Gly Phe Pro Tyr Leu Gly Gly Leu Pro Glu Ala Leu
 130 135 140

His Thr Pro Arg Arg Ala Val Pro Arg Thr Ser Val Pro Ala Gly Ser
 145 150 155 160

Val Gly Ile Gly Gly Ser Gln Thr Gly Val Tyr Pro Phe Ala Ser Pro
 165 170 175

Gly Gly Trp Gln Ile Ile Gly Arg Thr Glu Leu Pro Leu Phe Arg Ala
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Asp Leu Asn Pro Pro Thr Leu Leu Ala Ala Gly Asp Gln Val Arg Phe
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Val Ala Glu Arg Ile Glu Pro
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09330433-084501

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gga cgc tac gga cac cgg cgt tac ggc atc ggt cat gcc ggt gcg atg 96
Gly Arg Tyr Gly His Arg Arg Tyr Gly Ile Gly His Ala Gly Ala Met
          20             25             30

gac acg gtt gct ttg gcg gcg ggt aat att tta ttg ggc aac gac gaa 144
Asp Thr Val Ala Leu Ala Ala Gly Asn Ile Leu Leu Gly Asn Asp Glu
          35             40             45

ggc acg gcc gca atc gaa atc gct ttg ggc ggg ata atg ctg gtg ttt 192
Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe
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Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu
          65             70             75             80

ttg gac ggc gaa ccg gtc tat tgc tat tgg cgt tat acc gcc cgc aaa 288
Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys
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ggg cag acc ttg aaa atg gtg cgt gcc gtc cag ggc atg tac gcc tat 336
Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr
          100             105             110

gtg tgc gtg gcg ggc gga ttt gat gtg ccg gaa gtg atg ggt tgc aga 384
Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg
          115             120             125

agc acc gac ctg aaa gcc ggt ttc ggc ggc cat cag gcc aga atg ctg 432
Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu
          130             135             140

caa aaa ggc gat tat ctc ccc atc gcc aaa ggt gcg cag gaa ttg tcc 480
Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser
          145             150             155             160

aaa gtc ggc att gcc ccg ata ccg ttt acc gat acc atc cac ctt gtt 528
Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val
          165             170             175

cct tgc tgc gaa tat gcc gct ttc agt gaa aaa ggg cgt ctg aat ctg 576
Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu
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cgc ttc gac gga cag ccg ctg acc ctg tgg caa cct ttg gaa atg ctg	672
Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu	
210 215 220	
tcc cac gct gtt cag gca gga acc gtg cag gtg ccg ccc ggc ggc aaa	720
Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys	
225 230 235 240	
ccg att atc ctg ctg gcc gat gcg caa acc acc ggc ggt tat ccg aaa	768
Pro Ile Ile Leu Leu Ala Asp Ala Gln Thr Thr Gly Gly Tyr Pro Lys	
245 250 255	
atc gct acc gtt gcc gcc gcc gat ttg ggc agg ctg gca cag gtg cgc	816
Ile Ala Thr Val Ala Ala Ala Asp Leu Gly Arg Leu Ala Gln Val Arg	
260 265 270	
ttc ggc agc aaa gtc aaa ttc aaa ata atc ggc ttg aaa gaa gcc acc	864
Phe Gly Ser Lys Val Lys Phe Lys Ile Ile Gly Leu Lys Glu Ala Thr	
275 280 285	
gcc ctg cgg cgc aaa aac caa gtc tat ctg aac caa ata cgg aga atc	912
Ala Leu Arg Arg Lys Asn Gln Val Tyr Leu Asn Gln Ile Arg Arg Ile	
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 35 40 45
 Gly Thr Ala Ala Ile Glu Ile Ala Leu Gly Gly Ile Met Leu Val Phe
 50 55 60
 Glu Arg Asp Thr Pro Phe Cys Leu Thr Gly Ala Val Tyr Gln Ala Glu
 65 70 75 80
 Leu Asp Gly Glu Pro Val Tyr Ser Tyr Trp Arg Tyr Thr Ala Arg Lys
 85 90 95
 Gly Gln Thr Leu Lys Met Val Arg Ala Val Gln Gly Met Tyr Gly Tyr
 100 105 110

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Val Cys Val Ala Gly Gly Phe Asp Val Pro Glu Val Met Gly Ser Arg
 115 120 125

Ser Thr Asp Leu Lys Ala Gly Phe Gly Gly His Gln Gly Arg Met Leu
 130 135 140

Gln Lys Gly Asp Tyr Leu Pro Ile Gly Lys Gly Ala Gln Glu Leu Ser
 145 150 155 160

Lys Val Gly Ile Ala Pro Ile Pro Phe Thr Asp Thr Ile His Leu Val
 165 170 175

Pro Ser Ser Glu Tyr Ala Ala Phe Ser Glu Lys Gly Arg Leu Asn Leu
 180 185 190

Glu Arg Glu Thr Trp Thr Leu Gln Ser Asp Ser Asn Arg Met Gly Tyr
 195 200 205

Arg Phe Asp Gly Gln Pro Leu Thr Leu Ser Gln Pro Leu Glu Met Leu
 210 215 220

Ser His Ala Val Gln Ala Gly Thr Val Gln Val Pro Pro Gly Gly Lys
 225 230 235 240

Pro Ile Ile Leu Leu Ala Asp Ala Gln Thr Thr Gly Gly Tyr Pro Lys
 245 250 255

Ile Ala Thr Val Ala Ala Ala Asp Leu Gly Arg Leu Ala Gln Val Arg
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Phe Gly Ser Lys Val Lys Phe Lys Ile Ile Gly Leu Lys Glu Ala Thr
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 Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
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att tct gta ttt atg gtc ggc ttg ggt gta ggt ggc tat ttc ggt gga	192
Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly	
50 55 60	
cgc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc	240
Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile	
65 70 75 80	
gct gaa gta tcc atc ggt ctg ttc ggt ttg gta agc agg ggt ctg att	288
Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Arg Gly Leu Ile	
85 90 95	
tcc ggc ttg ggg cat ctt tta gtt gag gct gat ttg ccc atc atc gct	336
Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala	
100 105 110	
gct gcc aat ttc ctc tta ttg ctg ctt cct acc ttt atg atg ggc ggc	384
Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala	
115 120 125	
acc ttg ccc tgg ctg acc tgc ttt ttt aac cgg aaa ata cat aat gct	432
Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val	
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ggc gag tct atc ggt acc tta tat ttt ttc aac act ttg ggt ggc gca	480
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145 150 155 160	
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Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu	
165 170 175	
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Ser Gln Thr Ile Ala Leu Thr Ala Cys Phe Asn Leu Leu Ile Ala Ala	
180 185 190	
tca gta tgc tgc gtt aca gaa agg atg gat ata gtc aac act aaa ccg	624
Ser Val Cys Cys Val Thr Glu Arg Met Asp Ile Val Asn Thr Lys Pro	
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Asn Thr Ser Leu Ile Tyr Met Leu Ser Phe Leu Ser Gly Leu Leu Ser	
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225 230 235 240	
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Ser Val Pro Gln Ala Phe Ser Phe Thr Leu Ala Tyr Phe Leu Thr Gly	
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atc gcc gtc ggc ggc tat ttt ggc aaa cgg att tgc cgc agc cgc ttt	816
Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe	
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Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly	
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ttc gtc cac cac gcc ggt atc ttc att acc ctg tct gcc gtc gtc aga	960
Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg	
305 310 315 320	
ggg ttg att ttc ccg ctc gta cac cat gtg ggt acg gat ggc aac aaa	1008
Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys	
325 330 335	
tcc gga cga cag gtt tcc aat gtt tat ttc gcc aac gtt gcc ggc agt	1056
Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser	
340 345 350	
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Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Phe Leu Ser	
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acc caa cag att tac ctg ctc atc tgt ttg att tct gct gct gtc cct	1152
Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro	
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Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp	
405 410 415	
tct gtc ttt caa aat att gct gac cgt ccg gat ccg ctg att gaa aac	1296
Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn	
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aaa cac ggc att gtt gcg gtt tac cat aga gat ggt gat aag gtt gtt	1344
Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val	
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Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn	
450 455 460	
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Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser	
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ggc ata ccg ccg att ttc gtc gtt gga ttg agt aca ggt tgg tgg gcg	1488
Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala	
485 490 495	
cgc gtc ttg tct gcc att ccg gaa atg cag tgg atg atc gtt gcg gaa	1536
Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu	
500 505 510	

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Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala	
515 520 525	
ccg ctt ttg cag gac aaa cgt gtt gaa att gta ttg gat gac ggt agg	1632
Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg	
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Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met	
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Asn Thr Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala	
565 570 575	
gaa ttt tta aaa cag gtg caa agc cac ctt acc ccg gat ggt att gta	1776
Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val	
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atg ttt aat acc acg cac agc ccg cat gct ttt gct acc gcc gta cac	1824
Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His	
595 600 605	
agt att ccc tat gca tac cgc tat ggg cat atg gta gtc ggc tgc gca	1872
Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala	
610 615 620	
acc ccg gta gct ttc cct aat aaa gaa ctg ctc aag caa cgt ctc tcc	1920
Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser	
625 630 635 640	
ccc ttg att tgg ccg gaa agc ggc agg cac gta ttt gac agc agc acc	1968
Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr	
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Val Asp Ala Ala Ala Cln Lys Val Val Ser Arg Met Leu Ile Gln Met	
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acg gaa cct tgc gct ggg gcg gaa gtc att acc gac gat aat atg att	2064
Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile	
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 35 40 45
 Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly
 50 55 60
 Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile
 65 70 75 80
 Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Arg Gly Leu Ile
 85 90 95
 Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala
 100 105 110
 Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala
 115 120 125
 Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val
 130 135 140
 Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala
 145 150 155 160
 Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu
 165 170 175
 Ser Gln Thr Ile Ala Leu Thr Ala Cys Phe Asn Leu Leu Ile Ala Ala
 180 185 190
 Ser Val Cys Cys Val Thr Glu Arg Met Asp Ile Val Asn Thr Lys Pro
 195 200 205
 Asn Thr Ser Leu Ile Tyr Met Leu Ser Phe Leu Ser Gly Leu Leu Ser
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 Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln
 225 230 235 240
 Ser Val Pro Gln Ala Phe Ser Phe Thr Leu Ala Tyr Phe Leu Thr Gly
 245 250 255
 Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe
 260 265 270
 Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala
 275 280 285
 Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly
 290 295 300
 Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg
 305 310 315 320
 Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys
 325 330 335
 Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser
 340 345 350

093013 081604

Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Phe Leu Ser
355 360 365

Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro
370 375 380

Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser
385 390 395 400

Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp
405 410 415

Ser Val Phe Gln Asn Ile Ala Asp Arg Pro Asp Arg Leu Ile Glu Asn
420 425 430

Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val
435 440 445

Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Val Phe Asn
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Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser
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Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu
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515 520 525

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565 570 575

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580 585 590

Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His
595 600 605

Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala
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Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser
625 630 635 640

Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr
645 650 655

Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Gln Met
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Thr Glu Pro Ser Ala Gly Ala Glu Val Ile Thr Asp Asp Asn Met Ile
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35 40 45

Met Leu Cys Ala Gly Arg Asp Asp Val Ala Val Thr Asp Arg Asp Ala
50 55 60

Lys Ile Asn Ala Pro Pro Pro Asn Leu His Thr Gly Asp Phe Thr Asn
65 70 75 80

Pro Asn Asp Ala Tyr Lys Asn Leu Ile Asn Leu Lys Pro Ala Ile Glu
85 90 95

Ala Gly Tyr Thr Gly Arg Gly Val Glu Val Gly Ile Val Asp Thr Gly
100 105 110

Glu Ser Val Gly Ser Ile Ser Phe Pro Glu Leu Tyr Gly Arg Lys Glu
115 120 125

His Gly Tyr Asn Glu Asn Tyr Lys Asn Tyr Thr Ala Tyr Met Arg Lys
130 135 140

Glu Ala Pro Glu Asp Gly Gly Gly Lys Asp Ile Lys Ala Ser Phe Asp
145 150 155 160

Asp Glu Ala Val Ile Glu Thr Glu Ala Lys Pro Thr Asp Ile Arg His
165 170 175

Val Lys Glu Ile Gly His Ile Asp Val Val Ser His Ile Ile Gly Gly
180 185 190

Arg Ser Val Asp Gly Arg Pro Ala Gly Gly Ile Ala Pro Asp Ala Thr
195 200 205

Leu His Ile Met Asn Thr His Asp Gly Thr Lys Asn Glu Ile Met Ser
210 215 220

Ala Ala Ile Arg Asn Ala Trp Val Lys Leu Gly Glu Arg Gly Val Arg
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Ile Val Asn Asn Ser Phe Gly Thr Thr Ser Arg Ala Gly Thr Ala Asp
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His Phe Gln Ile Ala Asn Ser Glu Glu Gln Tyr Arg Gln Ala Leu Leu
260 265 270

Ala Tyr Ser Gly Gly Asp Lys Thr Asp Glu Gly Ile Arg Leu Met Gln
275 280 285

Gln Ser Asp Tyr Gly Asn Leu Ser Tyr His Ile Arg Asn Lys Asn Met
290 295 300

Leu Phe Ile Phe Ser Ala Ser Asn Asp Ala Gln Ala Gln Pro Asn Thr
305 310 315 320

Leu Thr Leu Leu Pro Phe Tyr Glu Lys Asp Ala Gln Lys Gly Ile Ile
325 330 335

Thr Val Ala Gly Val Asp Arg Ser Gly Glu Lys Phe Asn Gly Ser Asn
340 345 350

His Cys Gly Ile Thr Ala Met Trp Cys Leu Ser Ala Pro Tyr Glu Ala
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Ser Val Arg Phe Thr Arg Thr Asn Pro Ile Gln Ile Ala Gly Thr Ser
370 375 380

Phe Ser Ala Pro Ile Val Thr Gly Thr Ala Ala Leu Leu Leu Gln Lys
385 390 395 400

Tyr Pro Trp Met Ser Asn Asp Asn Leu Arg Thr Thr Leu Leu Thr Thr
405 410 415

Ala Gln Asp Ile Gly Ala Val Gly Val Asp Ser Lys Phe Gly Trp Gly
420 425 430

Leu Leu Asp Ala Gly Lys Ala Met Asn Gly Pro Ala Ser Phe Pro Phe
435 440 445

Gly Asp Phe Thr Ala Asp Thr Lys Gly Thr Ser Asp Ile Ala Tyr Ser
450 455 460

Phe Arg Asn Asp Ile Ser Gly Thr Gly Gly Leu Ile Lys Lys Gly Gly
465 470 475 480

Ser Gln Leu Gln Leu His Gly Asn Asn Thr Tyr Thr Gly Lys Thr Ile
485 490 495

Ile Glu Gly Gly Ser Leu Val Leu Tyr Gly Asn Asn Lys Ser Asp Met
500 505 510

Arg Val Glu Thr Lys Gly Ala Leu Ile Tyr Asn Gly Ala Ala Ser Gly
515 520 525

Gly Ser Leu Asn Ser Asp Gly Ile Val Tyr Leu Ala Asp Thr Asp Arg
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Ser Gly Ala Asn Glu Thr Val His Ile Lys Gly Asp Leu Gln Leu Gly
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09043 09160

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565 570 575

Gly Thr Ala Met Thr Gly Gly Lys Leu Tyr Met Ser Ala Arg Gly Lys
580 585 590

Gly Ala Gly Tyr Leu Asn Arg Thr Gly Gln Arg Val Pro Phe Leu Ser
595 600 605

Ala Ala Lys Ile Gly Arg Asp Tyr Ser Phe Phe Thr Asn Ile Glu Thr
610 615 620

Asp Gly Gly Leu Leu Ala Ser Leu Asp Ser Val Glu Lys Thr Ala Gly
625 630 635 640

Ser Glu Gly Asp Thr Leu Ser Tyr Tyr Val Arg Arg Gly Asn Ala Ala
645 650 655

Arg Thr Ala Ser Ala Ala Ala His Ser Ala Pro Ala Gly Leu Lys His
660 665 670

Ala Val Glu Gln Gly Gly Ser Asn Leu Glu Asn Leu Met Val Glu Leu
675 680 685

Asp Ala Ser Glu Ser Ser Ala Thr Pro Glu Thr Val Glu Thr Ala Ala
690 695 700

Ala Asp Arg Thr Asp Met Pro Gly Ile Arg Pro Tyr Gly Ala Thr Phe
705 710 715 720

Arg Ala Ala Ala Val Gln His Ala Asn Ala Ala Asp Gly Val Arg
725 730 735

Ile Phe Asn Ser Leu Ala Ala Thr Val Tyr Ala Asp Ser Thr Ala Ala
740 745 750

His Ala Asp Met Gln Gly Arg Arg Leu Lys Ala Val Ser Asp Gly Leu
755 760 765

Asp His Asn Ala Thr Gly Leu Arg Val Ile Ala Gln Thr Gln Gln Asp
770 775 780

Gly Gly Thr Trp Glu Gln Gly Gly Val Glu Gly Lys Met Arg Gly Ser
785 790 795 800

Thr Gln Thr Val Gly Ile Ala Ala Lys Thr Gly Glu Asn Thr Thr Ala
805 810 815

Ala Ala Thr Leu Gly Met Gly His Ser Thr Trp Ser Glu Asn Ser Ala
820 825 830

Asn Ala Lys Thr Asp Ser Ile Ser Leu Phe Ala Gly Ile Arg His Asp
835 840 845

Ala Gly Asp Ile Gly Tyr Leu Lys Gly Leu Phe Ser Tyr Gly Arg Tyr
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Lys Asn Ser Ile Ser Arg Ser Thr Gly Ala Asp Glu His Ala Glu Gly
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093043-081501

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1 5 10 15																
cat ttg ggt gta aag atg tat tcg cac act gtt cct gcg att gcc gag	96															
His Leu Gly Val Lys Met Tyr Ser His Thr Val Pro Ala Ile Ala Glu																
20 25 30																
ttg ata gcg aat gcc tac gat gca tgt gct acg gaa gtg gaa gtt agg	144															
Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg																
35 40 45																
tta ttc gat aaa ccg gag cat aaa atc gtt att aaa gat aat ggc ata	192															
Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile																
50 55 60																

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Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg	
65 70 75 80	
aac aga agg gaa gaa aaa caa gcc tcc ccg tgc gga aga att cca acg	288
Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr	
85 90 95	
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Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys	
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Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu	
115 120 125	
gat tat gca gag att aaa aaa agt gag cgt att tat caa ccg gag ttt	432
Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe	
130 135 140	
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Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr	
145 150 155 160	
tta acc gag ctg acg aaa aaa caa gga tac ccg tta gat aat tat gtg	528
Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val	
165 170 175	
ggg cat ctt tcc cgt tta ttt gat ttt ccg gct cag gat ttt aaa atc	576
Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile	
180 185 190	
aaa gta agc ttg aac ggc tgc gaa cca aga atc att gac gga aac cta	624
Lys Val Ser Leu Asn Gly Ser Glu Pro Arg Ile Ile Asp Gly Asn Leu	
195 200 205	
aaa tat aat ctt gtt acc cca caa ttc gaa tgg gaa tac cag gat cta	672
Lys Tyr Asn Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu	
210 215 220	
gca acc aat att tca tgc tta tct tca aaa ttc gaa cag tat gaa tac	720
Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr	
225 230 235 240	
agc gga tta ata caa ggt aag ttc att aca acg gaa aaa cct tta aag	768
Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys	
245 250 255	
aat aat atg aaa ggt att acc ttg ttt gcc aac ggc aga atg gta aat	816
Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn	
260 265 270	
atg ccc gag ttt ttc act gat agc gaa tcc agc cat ttc taa	858
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- <212> PRT
- <213> Neisseria gonorrhoeae

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Leu Ile Ala Asn Ala Tyr Asp Ala Cys Ala Thr Glu Val Glu Val Arg
      35           40           45

Leu Phe Asp Lys Pro Glu His Lys Ile Val Ile Lys Asp Asn Gly Ile
      50           55           60

Gly Met Ser Phe Asp Glu Ile Asn Asp Phe Tyr Leu Arg Ile Gly Arg
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Asn Arg Arg Glu Glu Lys Gln Ala Ser Pro Cys Gly Arg Ile Pro Thr
      85           90           95

Gly Lys Lys Gly Leu Gly Lys Leu Ala Leu Phe Arg Leu Gly Asn Lys
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Ile Glu Ile Ser Thr Ile Gln Gly Asn Glu Arg Val Thr Phe Thr Leu
      115           120           125

Asp Tyr Ala Glu Ile Lys Lys Ser Glu Arg Ile Tyr Gln Pro Glu Phe
      130           135           140

Gln Lys Glu Ser Val Lys Pro Asn Thr Glu Asn Gly Thr Thr Ile Thr
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Leu Thr Glu Leu Thr Lys Lys Gln Gly Tyr Pro Leu Asp Asn Tyr Val
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Gly His Leu Ser Arg Leu Phe Asp Phe Pro Ala Gln Asp Phe Lys Ile
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Lys Tyr Asn Leu Val Thr Pro Gln Phe Glu Trp Glu Tyr Gln Asp Leu
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Ala Thr Asn Ile Ser Ser Leu Ser Ser Lys Phe Glu Gln Tyr Glu Tyr
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Ser Gly Leu Ile Gln Gly Lys Phe Ile Thr Thr Glu Lys Pro Leu Lys
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Asn Asn Met Lys Gly Ile Thr Leu Phe Ala Asn Gly Arg Met Val Asn
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Met Pro Glu Phe Phe Thr Asp Ser Glu Ser Ser His Phe
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gcc agc gaa atc gcc tat cgc ttt gta ttc gga att gaa acc tta ccg	96
Ala Ser Glu Ile Ala Tyr Arg Phe Val Phe Gly Ile Glu Thr Leu Pro	
20 25 30	
gct gca aaa atg gcg gaa acg ttt gcg ctg aca ttt atg att gct gcg	144
Ala Ala Lys Met Ala Glu Thr Phe Ala Leu Thr Phe Met Ile Ala Ala	
35 40 45	
ctg tat ctg ttt gcg cgt tat aag gct tcg cgg ctg ctg att gcg gtg	192
Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val	
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Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr	
65 70 75 80	
caa agc tgg atg acg ggt att aac tat tgg ctg atg ctg aaa gag gtt	288
Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val	
85 90 95	
acc gaa gtc ggc agc gcg ggc gcg tcg atg ttg gat aag ttg tgg ctg	336
Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu	
100 105 110	
cct gct ttg tgg ggc gtg gcg gaa gtc atg ttg ttt tgc agc ctt gcc	384
Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala	
115 120 125	
aag ttc cgc cgt aag acg cat ttt tct gcc gat ata ctg ttt gcc ttc	432
Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe	
130 135 140	
cta atg ctg atg att ttc gtg cgt tcg ttc gac acg aaa caa gag cac	480
Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His	
145 150 155 160	
ggg att tcg ccc aaa ccg aca tac agc cgc atc aaa gcc aat tat ttc	528
Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe	
165 170 175	
agc ttc ggt tat ttt gtc ggg cgc gtg ttg ccg tat cag ttg ttt gat	576
Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp	
180 185 190	
tta agc aag atc cct gtg ttc aaa cag cct gct cca agc aaa atc ggg	624
Leu Ser Lys Ile Pro Val Phe Lys Gln Pro Ala Pro Ser Lys Ile Gly	

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gcg gcg cat ttg aaa ttg ttt ggt tac ggg cgc gaa act tcg ccg ttt Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe 225 230 235 240			720
tta acc cgg ctg tcg caa gcc gat ttt aag ccg att gtg aaa caa agt Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser 245 250 255			768
tat tcc gca ggc ttt atg acg gca gta tcc ctg ccc agt ttc ttt aac Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn 260 265 270			816
gtc ata ccg cac gcc aac ggc ttg gaa caa atc agc ggc ggc gat acc Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr 275 280 285			864
aac atg ttc cgc ctc gcc aaa gag cag ggc tat gaa acg tat ttt tac Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr 290 295 300			912
agt gcc cag gct gaa aac caa atg gca att ttg aac tta atc ggt aag Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys 305 310 315 320			960
aaa tgg ata gac cat ctg att cag ccg acg caa ctt ggc tac ggc aac Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn 325 330 335			1008
ggc gac aat atg ccc gat gag aag ctg ctg ccg ttg ttc gac aaa atc Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile 340 345 350			1056
aat ttg cag cag ggc agg cat ttt atc gtg ttg cac caa cgc ggt tcg Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser 355 360 365			1104
cac gcc cca tac ggc gca ttg ttg cag cct caa gat aaa gta ttc ggc His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly 370 375 380			1152
gaa gcc gat att gtg gat aag tac gac aac acc atc cac aaa acc gac Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp 385 390 395 400			1200
caa atg att caa acc gta ttc gag cag ctg caa aag cag cct gac ggc Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly 405 410 415			1248
aac tgg ctg ttt gcc tat acc tcc gat cat ggc cag tat gtg cgc caa Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln 420 425 430			1296
gat atc tac aat caa ggc acg gtg cag ccc gac agc tat att gtg cct Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro 435 440 445			1344

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Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln			
450	455	460	
gct ttt gcg cct tgc gag att gcc ttc cat cag cag ctt tca acg ttc			1440
Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe			
465	470	475	480
ctg att cac acg ttg ggc tac gat atg ccg gtt tca ggt tgt cgc gaa			1488
Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu			
	485	490	495
ggc tcg gta aca ggc aac ctg att acg gcc gat gca gcc agc ttg aac			1536
Gly Ser Val Thr Gly Asn Leu Ile Thr Gly Asp Ala Gly Ser Leu Asn			
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 35 40 45
 Leu Tyr Leu Phe Ala Arg Tyr Lys Ala Ser Arg Leu Leu Ile Ala Val
 50 55 60
 Phe Phe Ala Phe Ser Met Ile Ala Asn Asn Val His Tyr Ala Val Tyr
 65 70 75 80
 Gln Ser Trp Met Thr Gly Ile Asn Tyr Trp Leu Met Leu Lys Glu Val
 85 90 95
 Thr Glu Val Gly Ser Ala Gly Ala Ser Met Leu Asp Lys Leu Trp Leu
 100 105 110
 Pro Ala Leu Trp Gly Val Ala Glu Val Met Leu Phe Cys Ser Leu Ala
 115 120 125
 Lys Phe Arg Arg Lys Thr His Phe Ser Ala Asp Ile Leu Phe Ala Phe
 130 135 140
 Leu Met Leu Met Ile Phe Val Arg Ser Phe Asp Thr Lys Gln Glu His
 145 150 155 160
 Gly Ile Ser Pro Lys Pro Thr Tyr Ser Arg Ile Lys Ala Asn Tyr Phe

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Ser Phe Gly Tyr Phe Val Gly Arg Val Leu Pro Tyr Gln Leu Phe Asp 180	185	190
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Gln Gly Ser Ile Gln Asn Ile Val Leu Ile Met Gly Glu Ser Glu Ser 210	215	220
Ala Ala His Leu Lys Leu Phe Gly Tyr Gly Arg Glu Thr Ser Pro Phe 225	230	235
Leu Thr Arg Leu Ser Gln Ala Asp Phe Lys Pro Ile Val Lys Gln Ser 245	250	255
Tyr Ser Ala Gly Phe Met Thr Ala Val Ser Leu Pro Ser Phe Phe Asn 260	265	270
Val Ile Pro His Ala Asn Gly Leu Glu Gln Ile Ser Gly Gly Asp Thr 275	280	285
Asn Met Phe Arg Leu Ala Lys Glu Gln Gly Tyr Glu Thr Tyr Phe Tyr 290	295	300
Ser Ala Gln Ala Glu Asn Gln Met Ala Ile Leu Asn Leu Ile Gly Lys 305	310	315
Lys Trp Ile Asp His Leu Ile Gln Pro Thr Gln Leu Gly Tyr Gly Asn 325	330	335
Gly Asp Asn Met Pro Asp Glu Lys Leu Leu Pro Leu Phe Asp Lys Ile 340	345	350
Asn Leu Gln Gln Gly Arg His Phe Ile Val Leu His Gln Arg Gly Ser 355	360	365
His Ala Pro Tyr Gly Ala Leu Leu Gln Pro Gln Asp Lys Val Phe Gly 370	375	380
Glu Ala Asp Ile Val Asp Lys Tyr Asp Asn Thr Ile His Lys Thr Asp 385	390	395
Gln Met Ile Gln Thr Val Phe Glu Gln Leu Gln Lys Gln Pro Asp Gly 405	410	415
Asn Trp Leu Phe Ala Tyr Thr Ser Asp His Gly Gln Tyr Val Arg Gln 420	425	430
Asp Ile Tyr Asn Gln Gly Thr Val Gln Pro Asp Ser Tyr Ile Val Pro 435	440	445
Leu Val Leu Tyr Ser Pro Asp Lys Ala Val Gln Gln Ala Ala Asn Gln 450	455	460
Ala Phe Ala Pro Cys Glu Ile Ala Phe His Gln Gln Leu Ser Thr Phe 465	470	475
Leu Ile His Thr Leu Gly Tyr Asp Met Pro Val Ser Gly Cys Arg Glu		

09830433 084604

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 Leu Leu Thr Glu Lys Val Ser Pro Ile Ile Ala Leu Ile Leu Val Pro
 20 25 30
 ctg att ggg gcg ttg ctg gcg ggg ttt gat gta tcc caa tta aaa gaa 144
 Leu Ile Gly Ala Leu Leu Ala Gly Phe Asp Val Ser Gln Leu Lys Glu
 35 40 45
 ttt tat tgg ggc ggc acg aaa tgg gtg acg cag att gtg att atg ttt 192
 Phe Tyr Ser Gly Gly Thr Lys Ser Val Thr Gln Ile Val Ile Met Phe
 50 55 60
 atg ttt tcc att ttg ttt ttt gga atc atg aac gat gtg ggg ctg ttc 240
 Met Phe Ser Ile Leu Phe Phe Gly Ile Met Asn Asp Val Gly Leu Phe
 65 70 75 80
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 Arg Pro Met Ile Gly Gly Leu Ile Lys Leu Thr Arg Gly Asn Ile Val
 85 90 95
 gca gtg agt gtg ggg acg gtc ttg gtg tgg gtg gca cag ttg gac 336
 Ala Val Ser Val Gly Thr Val Leu Val Ser Val Val Ala Gln Leu Asp
 100 105 110
 ggg gcg ggc gcg acg acg ttt tta tgg gtc gtc ccc gcc ctt ttg ccg 384
 Gly Ala Gly Ala Thr Thr Phe Leu Ser Val Val Pro Ala Leu Leu Pro
 115 120 125
 ctt tac aag cgt ctg cat atg aat cct tac ctg ctg ttt ttg ctg ctg 432
 Leu Tyr Lys Arg Leu His Met Asn Pro Tyr Leu Leu Phe Leu Leu Leu
 130 135 140
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 Thr Ser Ser Ala Gly Leu Ile Asn Leu Leu Pro Arg Gly Gly Pro Ile
 145 150 155 160

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cct ttg ttg acg gtg caa att atc ggt gtg gtg ttt atc ctt gtg ctg	576
Pro Leu Leu Thr Val Gln Ile Ile Gly Val Val Phe Ile Leu Val Leu	
180 185 190	
tcc ctg ttt ttg ggt gtg cgt gaa aaa agg cgg att gtc cgg gag ttg	624
Ser Leu Phe Leu Gly Val Arg Glu Lys Arg Arg Ile Val Arg Glu Leu	
195 200 205	
ggc gcg ttg ccc gcc gtg gcg gat ttg ata aag ccg gcg cct ttg tgc	672
Gly Ala Leu Pro Ala Val Ala Asp Leu Ile Lys Pro Ala Pro Leu Ser	
210 215 220	
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Leu Leu Phe Leu Ala Ala Met Ser Leu Leu Phe Ser Gly Ile Phe Pro	
245 250 255	
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Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn	
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Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly	
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Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu	
290 295 300	
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Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu	
305 310 315 320	
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Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile	
325 330 335	
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Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly	
355 360 365	
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Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val	
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Leu	Ile	Gly	Ala	Leu	Leu	Ala	Gly	Phe	Asp	Val	Ser	Gln	Leu	Lys	Glu
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				85					90						95
Ala	Val	Ser	Val	Gly	Thr	Val	Leu	Val	Ser	Val	Val	Ala	Gln	Leu	Asp
			100					105					110		
Gly	Ala	Gly	Ala	Thr	Thr	Phe	Leu	Ser	Val	Val	Pro	Ala	Leu	Leu	Pro
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Leu	Tyr	Lys	Arg	Leu	His	Met	Asn	Pro	Tyr	Leu	Leu	Phe	Leu	Leu	Leu
	130					135					140				
Thr	Ser	Ser	Ala	Gly	Leu	Ile	Asn	Leu	Leu	Pro	Arg	Gly	Gly	Pro	Ile
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Gly	Arg	Val	Ala	Ser	Val	Leu	Gly	Ala	Asp	Val	Gly	Glu	Leu	Tyr	Lys
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			180					185					190		
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Gly	Ala	Leu	Pro	Ala	Val	Ala	Asp	Leu	Ile	Lys	Pro	Ala	Pro	Leu	Ser
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Glu Glu Glu Gln Lys Leu Ala Arg Pro Lys Leu Phe Trp Trp Asn Val
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 245 250 255

Pro Gly Tyr Val Phe Met Leu Ala Ala Thr Ala Ala Leu Leu Leu Asn
 260 265 270

Tyr Arg Ser Pro Gln Glu Gln Met Glu Arg Ile Tyr Ala His Ala Gly
 275 280 285

Gly Ala Val Met Met Ala Ser Ile Ile Leu Ala Ala Gly Thr Phe Leu
 290 295 300

Gly Ile Leu Lys Gly Ala Gly Met Leu Asp Ala Ile Ser Lys Asp Leu
 305 310 315 320

Val His Ile Leu Pro Asp Ala Leu Leu Pro Tyr Leu His Ile Ala Ile
 325 330 335

Gly Val Leu Gly Ile Pro Leu Glu Leu Val Leu Ser Thr Asp Ala Tyr
 340 345 350

Tyr Phe Gly Leu Phe Pro Ile Val Glu Gln Ile Thr Ser Gln Ala Gly
 355 360 365

Val Ala Pro Glu Ala Ala Gly Tyr Ala Met Leu Ile Gly Ser Ile Val
 370 375 380

Gly Thr Phe Val Thr Pro Leu Ser Pro Ala Leu Trp Met Gly Leu Gly
 385 390 395 400

Leu Ala Lys Leu Ser Met Gly Lys His Ile Arg Tyr Ser Phe Phe Trp
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Ile Val Pro Leu Pro
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act tat ctg tat caa aag ccc aag ctc ttc aaa gga gcg gtt cgg aat 96

0983043 081604

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ctc	gaa	gcc	gca	tct	tgt	aaa	tat	atc	aac	gag	ata	tac	caa	cga	gca	144
Leu	Glu	Ala	Ala	Ser	Cys	Lys	Tyr	Ile	Asn	Glu	Ile	Tyr	Gln	Arg	Ala	
		35					40					45				
gac	cca	acc	gca	cgc	ctg	ttt	cat	ctg	cgt	aaa	aaa	ggc	gca	atc	gtt	192
Asp	Pro	Thr	Ala	Pro	Leu	Phe	His	Leu	Arg	Lys	Lys	Gly	Ala	Ile	Val	
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cct	aaa	gaa	gaa	tac	gtc	gaa	agt	ttc	gac	gat	ttg	ggc	aaa	act	cgc	240
Pro	Lys	Glu	Glu	Tyr	Val	Glu	Ser	Phe	Asp	Asp	Leu	Gly	Lys	Thr	Arg	
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Tyr	Arg	Phe	Ile	Lys	Ser	Val	Ile	Tyr	Glu	His	Met	Lys	Asn	Gly	Ala	
				85					90					95		
tgc	tta	gtc	tat	aac	cat	att	aac	aac	gag	cgc	ttt	tca	gac	cat	atc	336
Ser	Leu	Val	Tyr	Asn	His	Ile	Asn	Asn	Glu	Pro	Phe	Ser	Asp	His	Ile	
			100					105					110			
gcc	cgt	caa	gtc	gcc	cgc	ttt	gcc	ggc	gca	cat	act	att	gtt	agt	gga	384
Ala	Arg	Gln	Val	Ala	Arg	Phe	Ala	Gly	Ala	His	Thr	Ile	Val	Ser	Gly	
		115					120					125				
tat	ctt	gct	ttt	ggc	agg	gac	gaa	tct	tat	aaa	aac	cat	tgg	gat	acc	432
Tyr	Leu	Ala	Phe	Gly	Ser	Asp	Glu	Ser	Tyr	Lys	Asn	His	Trp	Asp	Thr	
		130				135					140					
cgc	gat	gtg	tat	gcc	atc	cag	ctt	ttc	ggc	aag	aaa	cgt	tgg	caa	ctt	480
Arg	Asp	Val	Tyr	Ala	Ile	Gln	Leu	Phe	Gly	Lys	Lys	Arg	Trp	Gln	Leu	
		145				150				155					160	
act	goc	cct	gat	ttc	cct	atg	cca	ttg	tat	atg	caa	cag	act	aaa	gat	528
Thr	Ala	Pro	Asp	Phe	Pro	Met	Pro	Leu	Tyr	Met	Gln	Gln	Thr	Lys	Asp	
				165				170					175			
act	gat	att	tcc	att	cct	gaa	cat	atc	gat	atg	gat	att	atc	ctt	gaa	576
Thr	Asp	Ile	Ser	Ile	Pro	Glu	His	Ile	Asp	Met	Asp	Ile	Ile	Leu	Glu	
			180					185					190			
gca	ggg	gat	gtc	ctc	tac	atc	cca	cgc	ggg	tgg	tgg	cac	aga	cct	atc	624
Ala	Gly	Asp	Val	Leu	Tyr	Ile	Pro	Arg	Gly	Trp	Trp	His	Arg	Pro	Ile	
		195					200					205				
cgc	ctc	ggc	tgt	gaa	acc	ttc	cac	ttc	gct	gtc	ggg	acc	ttc	cca	cca	672
Pro	Leu	Gly	Cys	Glu	Thr	Phe	His	Phe	Ala	Val	Gly	Thr	Phe	Pro	Pro	
		210				215					220					
aac	ggc	tat	aat	tac	ctc	gag	tgg	cta	atg	aag	aaa	ttt	ccc	acc	ata	720
Asn	Gly	Tyr	Asn	Tyr	Leu	Glu	Trp	Leu	Met	Lys	Lys	Phe	Pro	Thr	Ile	
		225				230				235					240	
gaa	agt	ctg	cgc	cac	agt	ttc	tca	gac	tgg	gag	caa	gat	agg	acg	cgt	768
Glu	Ser	Leu	Arg	His	Ser	Phe	Ser	Asp	Trp	Glu	Gln	Asp	Arg	Thr	Arg	
				245				250					255			
atc	aac	gat	act	gcc	gca	caa	att	gct	gcc	atg	att	gcc	gac	ccc	gtc	816

109180 109180 109180

Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val	
260 265 270	
aat tat gaa gcc ttc agt gaa gac ttt ctc ggc aaa gaa cgt acc gat	864
Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp	
275 280 285	
acc gct ttt cat ctc gaa cag ttc gcg aat ccc aac gct act ccg ctt	912
Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu	
290 295 300	
tca gac gac gtc agg ttg aga tta aat gcc aat aat ttg gat acg ttg	960
Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu	
305 310 315 320	
gaa aag gga tat ttg att ggg aat ggg atg aag ata agc gta gat gag	1008
Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu	
325 330 335	
ttg ggg aaa aaa gtg tta gaa cac atc ggt aag aat gaa ccg tta ttg	1056
Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu	
340 345 350	
ttg aaa aat cta ctg gtt aac ttc aat cag gca aaa cat gaa gaa gtt	1104
Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Ala Lys His Glu Glu Val	
355 360 365	
agg aag ttg atc tat cag ttg ata gag tta gat ttt ctg gaa att ttg	1152
Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Ile Leu	
370 375 380	
tga	1155

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 <212> PRT
 <213> Neisseria gonorrhoeae

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Thr Tyr Leu Tyr Gln Lys Pro Lys Leu Phe Lys Gly Ala Val Arg Asn
20 25 30
Leu Glu Ala Ala Ser Cys Lys Tyr Ile Asn Glu Ile Tyr Gln Arg Ala
35 40 45
Asp Pro Thr Ala Pro Leu Phe His Leu Arg Lys Lys Gly Ala Ile Val
50 55 60
Pro Lys Glu Glu Tyr Val Glu Ser Phe Asp Asp Leu Gly Lys Thr Arg
65 70 75 80
Tyr Arg Phe Ile Lys Ser Val Ile Tyr Glu His Met Lys Asn Gly Ala
85 90 95
Ser Leu Val Tyr Asn His Ile Asn Asn Glu Pro Phe Ser Asp His Ile
100 105 110

09030433.084604

Ala Arg Gln Val Ala Arg Phe Ala Gly Ala His Thr Ile Val Ser Gly
115 120 125

Tyr Leu Ala Phe Gly Ser Asp Glu Ser Tyr Lys Asn His Trp Asp Thr
130 135 140

Arg Asp Val Tyr Ala Ile Gln Leu Phe Gly Lys Lys Arg Trp Gln Leu
145 150 155 160

Thr Ala Pro Asp Phe Pro Met Pro Leu Tyr Met Gln Gln Thr Lys Asp
165 170 175

Thr Asp Ile Ser Ile Pro Glu His Ile Asp Met Asp Ile Ile Leu Glu
180 185 190

Ala Gly Asp Val Leu Tyr Ile Pro Arg Gly Trp Trp His Arg Pro Ile
195 200 205

Pro Leu Gly Cys Glu Thr Phe His Phe Ala Val Gly Thr Phe Pro Pro
210 215 220

Asn Gly Tyr Asn Tyr Leu Glu Trp Leu Met Lys Lys Phe Pro Thr Ile
225 230 235 240

Glu Ser Leu Arg His Ser Phe Ser Asp Trp Glu Gln Asp Arg Thr Arg
245 250 255

Ile Asn Asp Thr Ala Ala Gln Ile Ala Ala Met Ile Ala Asp Pro Val
260 265 270

Asn Tyr Glu Ala Phe Ser Glu Asp Phe Leu Gly Lys Glu Arg Thr Asp
275 280 285

Thr Ala Phe His Leu Glu Gln Phe Ala Asn Pro Asn Ala Thr Pro Leu
290 295 300

Ser Asp Asp Val Arg Leu Arg Leu Asn Ala Asn Asn Leu Asp Thr Leu
305 310 315 320

Glu Lys Gly Tyr Leu Ile Gly Asn Gly Met Lys Ile Ser Val Asp Glu
325 330 335

Leu Gly Lys Lys Val Leu Glu His Ile Gly Lys Asn Glu Pro Leu Leu
340 345 350

Leu Lys Asn Leu Leu Val Asn Phe Asn Gln Ala Lys His Glu Glu Val
355 360 365

Arg Lys Leu Ile Tyr Gln Leu Ile Glu Leu Asp Phe Leu Glu Ile Leu
370 375 380

- <210> 62
- <211> 717
- <212> DNA
- <213> Neisseria meningitidis
- <220>

0930433 031501

<221> CDS

<222> (1) .. (714)

<400> 62

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  1             5             10             15

cgc caa acc agc ctg acg ggt aaa gtg att ctg aca cga ccg ttg tca 96
Arg Gln Thr Ser Leu Thr Gly Lys Val Ile Leu Thr Arg Pro Leu Ser
          20             25             30

ttt tcc cta tgg acg aca ttt gca tcg ata tct gcg tta ttg att atc 144
Phe Ser Leu Trp Thr Thr Phe Ala Ser Ile Ser Ala Leu Leu Ile Ile
          35             40             45

ctg ttt ttg ata ttt ggt aac tat acg cga aag aca aca gtg gag gga 192
Leu Phe Leu Ile Phe Gly Asn Tyr Thr Arg Lys Thr Thr Val Glu Gly
          50             55             60

caa att tta cct gca tcg gcc gta atc agg gtg tat gca ccg gat acg 240
Gln Ile Leu Pro Ala Ser Gly Val Ile Arg Val Tyr Ala Pro Asp Thr
          65             70             75             80

ggg aca att aca gcg aaa ttc gtg gaa gat gga gaa aag gtt aag gct 288
Gly Thr Ile Thr Ala Lys Phe Val Glu Asp Gly Glu Lys Val Lys Ala
          85             90             95

ggc gac aag cta ttt gcg ctt tcg acc tca cgt ttc gcc gca gga gat 336
Gly Asp Lys Leu Phe Ala Leu Ser Thr Ser Arg Phe Gly Ala Gly Asp
          100             105             110

agc gtg cag cag cag ttg aaa acg gag gca gtt ttg aag aaa acg ttg 384
Ser Val Gln Gln Gln Leu Lys Thr Glu Ala Val Leu Lys Lys Thr Leu
          115             120             125

gca gaa cag gaa ctg ggt cgt ctg aag ctg ata cac ggg aat gaa acg 432
Ala Glu Gln Glu Leu Gly Arg Leu Lys Leu Ile His Gly Asn Glu Thr
          130             135             140

cgc agc ctt aaa gca act gtc gaa cgt ttg gaa aac cag gaa ctc cat 480
Arg Ser Leu Lys Ala Thr Val Glu Arg Leu Glu Asn Gln Glu Leu His
          145             150             155             160

att tcg caa cag ata gac ggt cag aaa agg cgc att aga ctt gcg gaa 528
Ile Ser Gln Gln Ile Asp Gly Gln Lys Arg Arg Ile Arg Leu Ala Glu
          165             170             175

gaa atg ttg cag aaa tat cgt ttc cta tcc gcc aat gat gca gtg cca 576
Glu Met Leu Gln Lys Tyr Arg Phe Leu Ser Ala Asn Asp Ala Val Pro
          180             185             190

aaa caa gaa atg atg aat gtc aag gca gag ctt tta gag cag aaa gcc 624
Lys Gln Glu Met Met Asn Val Lys Ala Glu Leu Leu Glu Gln Lys Ala
          195             200             205

aaa ctt gat gcc tac cgc cga gaa gaa gtc ggg ctg ctt cag gaa atc 672
Lys Leu Asp Ala Tyr Arg Arg Glu Glu Val Gly Leu Leu Gln Glu Ile
          210             215             220

cgc acg cag aat ctg aca ttg gcc agc ctc ccc caa gcg gca tga 717
Arg Thr Gln Asn Leu Thr Leu Ala Ser Leu Pro Gln Ala Ala
          225             230             235

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<210> 63

09830433-081604

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Arg	Gln	Thr	Ser	Leu	Thr	Gly	Lys	Val	Ile	Leu	Thr	Arg	Pro	Leu	Ser	
			20					25					30			
Phe	Ser	Leu	Trp	Thr	Thr	Phe	Ala	Ser	Ile	Ser	Ala	Leu	Leu	Ile	Ile	
		35					40					45				
Leu	Phe	Leu	Ile	Phe	Gly	Asn	Tyr	Thr	Arg	Lys	Thr	Thr	Val	Glu	Gly	
	50					55					60					
Gln	Ile	Leu	Pro	Ala	Ser	Gly	Val	Ile	Arg	Val	Tyr	Ala	Pro	Asp	Thr	
65					70					75					80	
Gly	Thr	Ile	Thr	Ala	Lys	Phe	Val	Glu	Asp	Gly	Glu	Lys	Val	Lys	Ala	
				85					90					95		
Gly	Asp	Lys	Leu	Phe	Ala	Leu	Ser	Thr	Ser	Arg	Phe	Gly	Ala	Gly	Asp	
		100						105					110			
Ser	Val	Gln	Gln	Gln	Leu	Lys	Thr	Glu	Ala	Val	Leu	Lys	Lys	Thr	Leu	
	115						120					125				
Ala	Glu	Gln	Glu	Leu	Gly	Arg	Leu	Lys	Leu	Ile	His	Gly	Asn	Glu	Thr	
130						135					140					
Arg	Ser	Leu	Lys	Ala	Thr	Val	Glu	Arg	Leu	Glu	Asn	Gln	Glu	Leu	His	
145					150					155					160	
Ile	Ser	Gln	Gln	Ile	Asp	Gly	Gln	Lys	Arg	Arg	Ile	Arg	Leu	Ala	Glu	
			165						170					175		
Glu	Met	Leu	Gln	Lys	Tyr	Arg	Phe	Leu	Ser	Ala	Asn	Asp	Ala	Val	Pro	
		180						185					190			
Lys	Gln	Glu	Met	Met	Asn	Val	Lys	Ala	Glu	Leu	Leu	Glu	Gln	Lys	Ala	
	195						200					205				
Lys	Leu	Asp	Ala	Tyr	Arg	Arg	Glu	Glu	Val	Gly	Leu	Leu	Gln	Glu	Ile	
210					215						220					
Arg	Thr	Gln	Asn	Leu	Thr	Leu	Ala	Ser	Leu	Pro	Gln	Ala	Ala			
225					230					235						

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<211> 690
<212> DNA
<213> Neisseria meningitidis
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<220>

<222> (1) .. (687)

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Met	Met	Asn	Val	Glu	Ala	Glu	Leu	Leu	Glu	Gln	Lys	Ala	Lys	Leu	Asp	
1				5					10					15		
gcc	tac	ggc	cga	gaa	gaa	gcc	ggg	ctg	ctt	cag	gaa	atc	cgc	acg	cag	96
Ala	Tyr	Gly	Arg	Glu	Glu	Ala	Gly	Leu	Leu	Gln	Glu	Ile	Arg	Thr	Gln	
			20					25					30			
aat	ctg	aca	ttg	gcc	agc	ctc	ccc	aaa	cgg	cat	gag	aca	gaa	caa	agc	144
Asn	Leu	Thr	Leu	Ala	Ser	Leu	Pro	Lys	Arg	His	Glu	Thr	Glu	Gln	Ser	
		35					40					45				
cag	ctt	gaa	cgc	acc	atg	gcc	gat	att	tct	caa	gaa	gtt	ttg	gat	ttt	192
Gln	Leu	Glu	Arg	Thr	Met	Ala	Asp	Ile	Ser	Gln	Glu	Val	Leu	Asp	Phe	
	50					55					60					
gaa	atg	cgc	tct	gaa	caa	atc	atc	cgt	gca	gga	cgg	tcg	ggc	tat	ata	240
Glu	Met	Arg	Ser	Glu	Gln	Ile	Ile	Arg	Ala	Gly	Arg	Ser	Gly	Tyr	Ile	
65					70				75						80	
gca	ata	cgc	aac	gtc	gaa	gtc	gga	cgg	cag	gtt	gat	cct	tcc	aaa	ctg	288
Ala	Ile	Pro	Asn	Val	Glu	Val	Gly	Arg	Gln	Val	Asp	Pro	Ser	Lys	Leu	
				85					90					95		
ctc	ttg	agc	att	gtt	ccc	gaa	cgt	acc	gag	tta	tat	gcc	cat	cta	tat	336
Leu	Leu	Ser	Ile	Val	Pro	Glu	Arg	Thr	Glu	Leu	Tyr	Ala	His	Leu	Tyr	
			100					105					110			
atc	ccc	agc	agt	gca	gca	ggc	ttt	atc	aag	ccg	aaa	gac	aag	gtt	gtc	384
Ile	Pro	Ser	Ser	Ala	Ala	Gly	Phe	Ile	Lys	Pro	Lys	Asp	Lys	Val	Val	
		115					120					125				
cta	cgt	tat	cag	gca	tat	ccc	tat	cag	aaa	ttc	ggg	ctt	gct	tcc	ggc	432
Leu	Arg	Tyr	Gln	Ala	Tyr	Pro	Tyr	Gln	Lys	Phe	Gly	Leu	Ala	Ser	Gly	
	130					135					140					
agt	gtc	gta	tca	gtg	gca	aaa	acg	gca	ctg	ggc	aga	cag	gaa	ttg	tcg	480
Ser	Val	Val	Ser	Val	Ala	Lys	Thr	Ala	Leu	Gly	Arg	Gln	Glu	Leu	Ser	
145					150					155					160	
gga	ttg	ggc	atg	gta	tcc	tcc	gat	ttg	gcg	aag	agc	aac	gaa	cct	gtt	528
Gly	Leu	Gly	Met	Val	Ser	Ser	Asp	Leu	Ala	Lys	Ser	Asn	Glu	Pro	Val	
				165					170					175		
tat	ctc	gtg	aaa	ata	aaa	ccc	gac	aaa	cca	acc	atc	act	gca	tac	ggc	576
Tyr	Leu	Val	Lys	Ile	Lys	Pro	Asp	Lys	Pro	Thr	Ile	Thr	Ala	Tyr	Gly	
			180					185					190			
gag	gaa	aaa	cgc	ctg	caa	atc	ggc	atg	acg	ctg	gaa	gca	gac	atc	cta	624
Glu	Glu	Lys	Pro	Leu	Gln	Ile	Gly	Met	Thr	Leu	Glu	Ala	Asp	Ile	Leu	
		195					200					205				
cac	gag	aaa	cgg	cgg	ctg	tac	gaa	tgg	gta	ttg	gag	ccg	att	t		

<210> 65
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 <212> PRT
 <213> Neisseria gonorrhoeae

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 1 5 10 15
 Ala Tyr Gly Arg Glu Glu Ala Gly Leu Leu Gln Glu Ile Arg Thr Gln
 20 25 30
 Asn Leu Thr Leu Ala Ser Leu Pro Lys Arg His Glu Thr Glu Gln Ser
 35 40 45
 Gln Leu Glu Arg Thr Met Ala Asp Ile Ser Gln Glu Val Leu Asp Phe
 50 55 60
 Glu Met Arg Ser Glu Gln Ile Ile Arg Ala Gly Arg Ser Gly Tyr Ile
 65 70 75 80
 Ala Ile Pro Asn Val Glu Val Gly Arg Gln Val Asp Pro Ser Lys Leu
 85 90 95
 Leu Leu Ser Ile Val Pro Glu Arg Thr Glu Leu Tyr Ala His Leu Tyr
 100 105 110
 Ile Pro Ser Ser Ala Ala Gly Phe Ile Lys Pro Lys Asp Lys Val Val
 115 120 125
 Leu Arg Tyr Gln Ala Tyr Pro Tyr Gln Lys Phe Gly Leu Ala Ser Gly
 130 135 140
 Ser Val Val Ser Val Ala Lys Thr Ala Leu Gly Arg Gln Glu Leu Ser
 145 150 155 160
 Gly Leu Gly Met Val Ser Ser Asp Leu Ala Lys Ser Asn Glu Pro Val
 165 170 175
 Tyr Leu Val Lys Ile Lys Pro Asp Lys Pro Thr Ile Thr Ala Tyr Gly
 180 185 190
 Glu Glu Lys Pro Leu Gln Ile Gly Met Thr Leu Glu Ala Asp Ile Leu
 195 200 205
 His Glu Lys Arg Arg Leu Tyr Glu Trp Val Leu Glu Pro Ile Tyr Ser
 210 215 220
 Met Ser Gly Arg Leu
 225

<210> 66
 <211> 924
 <212> DNA
 <213> Neisseria gonorrhoeae

<220>

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Met	Gln	Tyr	Ser	Thr	Leu	Ala	Gly	Gln	Thr	Asp	Asn	Ser	Leu	Val	Ser	
1				5					10					15		
aat	aat	ttc	ggg	ttt	ttg	cgc	ctg	cgg	ctt	aat	ttt	atg	cgg	tat	gaa	96
Asn	Asn	Phe	Gly	Phe	Leu	Arg	Leu	Pro	Leu	Asn	Phe	Met	Pro	Tyr	Glu	
			20					25					30			
agc	cat	gcc	gat	tgg	gtt	att	acc	ggc	gtg	cct	tat	gat	atg	gcg	gtt	144
Ser	His	Ala	Asp	Trp	Val	Ile	Thr	Gly	Val	Pro	Tyr	Asp	Met	Ala	Val	
		35					40					45				
tca	ggg	cgt	tcc	ggc	gcg	cgt	ttc	ggc	cct	gaa	gcc	atc	cgg	cgc	gcc	192
Ser	Gly	Arg	Ser	Gly	Ala	Arg	Phe	Gly	Pro	Glu	Ala	Ile	Arg	Arg	Ala	
	50					55					60					
tcc	gtc	aac	ctc	gct	tgg	gag	cac	cgc	agg	ttt	cgg	tgg	aca	ttt	gat	240
Ser	Val	Asn	Leu	Ala	Trp	Glu	His	Arg	Arg	Phe	Pro	Trp	Thr	Phe	Asp	
65					70				75						80	
gtg	cgc	gaa	cgc	ctg	aac	att	att	gat	tgc	ggc	gac	tgg	gtt	ttt	tct	288
Val	Arg	Glu	Arg	Leu	Asn	Ile	Ile	Asp	Cys	Gly	Asp	Leu	Val	Phe	Ser	
				85					90					95		
ttt	ggc	gac	agc	agg	gat	ttt	gtc	gaa	aaa	atg	gaa	gcg	cac	gcc	ggc	336
Phe	Gly	Asp	Ser	Arg	Asp	Phe	Val	Glu	Lys	Met	Glu	Ala	His	Ala	Gly	
			100					105					110			
aaa	tta	ctt	tct	tcc	ggc	aaa	cgc	tgt	tgg	agt	tgg	ggc	ggc	gac	cat	384
Lys	Leu	Leu	Ser	Phe	Gly	Lys	Arg	Cys	Leu	Ser	Leu	Gly	Gly	Asp	His	
		115					120					125				
ttc	att	acc	ctc	cgg	ttg	ttg	cgc	gcc	cac	gcc	cgc	tat	ttc	ggc	aaa	432
Phe	Ile	Thr	Leu	Pro	Leu	Leu	Arg	Ala	His	Ala	Arg	Tyr	Phe	Gly	Lys	
		130				135					140					
ctc	gca	ctg	att	cat	ttt	gac	ggg	cac	acc	gac	acc	tac	gac	aac	ggc	480
Leu	Ala	Leu	Ile	His	Phe	Asp	Ala	His	Thr	Asp	Thr	Tyr	Asp	Asn	Gly	
145					150					155					160	
agc	gaa	tac	gac	cac	ggc	acg	atg	ttt	tat	acc	gcc	ccc	aag	gaa	ggc	528
Ser	Glu	Tyr	Asp	His	Gly	Thr	Met	Phe	Tyr	Thr	Ala	Pro	Lys	Glu	Gly	
				165				170						175		
ctc	atc	gac	cgg	tcc	cgt	tcc	gta	caa	atc	ggc	ata	cgc	acc	gaa	cac	576
Leu	Ile	Asp	Pro	Ser	Arg	Ser	Val	Gln	Ile	Gly	Ile	Arg	Thr	Glu	His	
			180					185					190			

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agt aaa aaa ttg cct ttt act gtg ttg tcc gcc ccc aaa gtc aat gaa 624
Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu
      195                200                205

gac agt gtt gaa gag acc gtc cgt aaa atc aaa gaa acc gtc ggc aat 672
Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
      210                215                220

atg ccc gtt tac ctg act ttc gac ata gac tgt ctc gac ccg tcg ttc 720
Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
      225                230                235                240

gcc ccc ggg acc ggt acg ccc gta tgc ggc ggc ttg agc agc gac agg 768
Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg
      245                250                255

gca tta aaa atc cta cgt ggg ctg acg gat ctc gac atc gtc ggt atg 816
Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met
      260                265                270

gat gtt gta gaa gtt gcc ccc tct tac gac caa tcc gac att acc gct 864
Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
      275                280                285

ttg gcc ggc gcc aca att gcc ttg gaa atg ctt tac ctt caa ggt gcg 912
Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Gln Gly Ala
      290                295                300

aaa aag gac tga 924
Lys Lys Asp
      305

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<210> 67

<211> 307

<212> PRT

<213> Neisseria gonorrhoeae

<400> 67

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Met Gln Tyr Ser Thr Leu Ala Gly Gln Thr Asp Asn Ser Leu Val Ser
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Asn Asn Phe Gly Phe Leu Arg Leu Pro Leu Asn Phe Met Pro Tyr Glu
      20                25                30

Ser His Ala Asp Trp Val Ile Thr Gln Val Pro Tyr Asp Met Ala Val
      35                40                45

Ser Gly Arg Ser Gly Ala Arg Phe Gly Pro Glu Ala Ile Arg Arg Ala
      50                55                60

Ser Val Asn Leu Ala Trp Glu His Arg Arg Phe Pro Trp Thr Phe Asp
      65                70                75                80

Val Arg Glu Arg Leu Asn Ile Ile Asp Cys Gly Asp Leu Val Phe Ser
      85                90                95

Phe Gly Asp Ser Arg Asp Phe Val Glu Lys Met Glu Ala His Ala Gly
      100                105                110

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05830433.081604

Lys Leu Leu Ser Phe Gly Lys Arg Cys Leu Ser Leu Gly Gly Asp His
 115 120 125

Phe Ile Thr Leu Pro Leu Leu Arg Ala His Ala Arg Tyr Phe Gly Lys
 130 135 140

Leu Ala Leu Ile His Phe Asp Ala His Thr Asp Thr Tyr Asp Asn Gly
 145 150 155 160

Ser Glu Tyr Asp His Gly Thr Met Phe Tyr Thr Ala Pro Lys Glu Gly
 165 170 175

Leu Ile Asp Pro Ser Arg Ser Val Gln Ile Gly Ile Arg Thr Glu His
 180 185 190

Ser Lys Lys Leu Pro Phe Thr Val Leu Ser Ala Pro Lys Val Asn Glu
 195 200 205

Asp Ser Val Glu Glu Thr Val Arg Lys Ile Lys Glu Thr Val Gly Asn
 210 215 220

Met Pro Val Tyr Leu Thr Phe Asp Ile Asp Cys Leu Asp Pro Ser Phe
 225 230 235 240

Ala Pro Gly Thr Gly Thr Pro Val Cys Gly Gly Leu Ser Ser Asp Arg
 245 250 255

Ala Leu Lys Ile Leu Arg Gly Leu Thr Asp Leu Asp Ile Val Gly Met
 260 265 270

Asp Val Val Glu Val Ala Pro Ser Tyr Asp Gln Ser Asp Ile Thr Ala
 275 280 285

Leu Ala Gly Ala Thr Ile Ala Leu Glu Met Leu Tyr Leu Cln Gly Ala
 290 295 300

Lys Lys Asp
 305

<210> 68
 <211> 1404
 <212> DNA
 <213> Neisseria meningitidis

<220>
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 <222> (1)..(1401)

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tgc ctg aca ctg acg ccc tac ttg caa cat gaa cta ttt tcc gct atg 96
 Cys Leu Thr Leu Thr Pro Tyr Leu Gln His Glu Leu Phe Ser Ala Met
 20 25 30

aaa tcc tat ttt tcc aaa tat atc cta ccc gtt tca ctt ttt acc ttg 144

0033033.0360

Lys Ser Tyr Phe Ser Lys Tyr Ile Leu Pro Val Ser Leu Phe Thr Leu	
35 40 45	
cca cta tcc ett tcc cca tcc gtt tgg gct ttt acg ctg cct gaa gca	192
Pro Leu Ser Leu Ser Pro Ser Val Ser Ala Phe Thr Leu Pro Glu Ala	
50 55 60	
tgg cgg gcg gcg cag caa cat tgg gct gat ttt caa gcg tcc cat tac	240
Trp Arg Ala Ala Gln Gln His Ser Ala Asp Phe Gln Ala Ser His Tyr	
65 70 75 80	
cag cgt gat gca gtg cgc gca cgg caa caa caa gcc aag gcc gca ttc	288
Gln Arg Asp Ala Val Arg Ala Arg Gln Gln Gln Ala Lys Ala Ala Phe	
85 90 95	
ctt ccc cat gta tcc gcc aat gcc agc tac cag cgc cag ccg cca tgg	336
Leu Pro His Val Ser Ala Asn Ala Ser Tyr Gln Arg Gln Pro Pro Ser	
100 105 110	
att tct tcc acc cgc gaa aca cag gga tgg agc gtg cag gtg gga caa	384
Ile Ser Ser Thr Arg Glu Thr Gln Gly Trp Ser Val Gln Val Gly Gln	
115 120 125	
acc tta ttt gac gcc gcc aaa ttt gca caa tac cgc caa agc agg ttc	432
Thr Leu Phe Asp Ala Ala Lys Phe Ala Gln Tyr Arg Gln Ser Arg Phe	
130 135 140	
gac acg cag gct gca gaa cag cgt ttc gat gcg gca cgc gaa gaa ttg	480
Asp Thr Gln Ala Ala Glu Gln Arg Phe Asp Ala Ala Arg Glu Glu Leu	
145 150 155 160	
ctg ttg aaa gct gcc gaa agt tat ttc aac gtt tta ctg agc cga gac	528
Leu Leu Lys Val Ala Glu Ser Tyr Phe Asn Val Leu Leu Ser Arg Asp	
165 170 175	
acc gtt gcc gcc cat gcg gcg gaa aaa gag gct tat gcc cag cag gta	576
Thr Val Ala Ala His Ala Ala Glu Lys Glu Ala Tyr Ala Gln Gln Val	
180 185 190	
agg cag gcg cag gct tta ttc aat aaa ggt gct gcc acc gcg ctg gat	624
Arg Gln Ala Gln Ala Leu Phe Asn Lys Gly Ala Ala Thr Ala Leu Asp	
195 200 205	
att cac gaa gcc aaa gcc ggt tac gac aat gcc ctg gcc caa gaa atc	672
Ile His Glu Ala Lys Ala Gly Tyr Asp Asn Ala Leu Ala Gln Glu Ile	
210 215 220	
gcc gta ttg gct gag aaa caa acc aat gaa aac cag ttg aac gac tac	720
Ala Val Leu Ala Glu Lys Gln Thr Tyr Glu Asn Gln Leu Asn Asp Tyr	
225 230 235 240	
acc gac ctg gat agc aaa caa atc gag gcc ata gat acc gcc aac ctg	768
Thr Asp Leu Asp Ser Lys Gln Ile Glu Ala Ile Asp Thr Ala Asn Leu	
245 250 255	
ttg gca cgc tat ctg ccc aag ctg gaa cgt tac agt ctg gat gaa tgg	816
Leu Ala Arg Tyr Leu Pro Lys Leu Glu Arg Tyr Ser Leu Asp Glu Trp	
260 265 270	
cag cgc att gcc tta tcc aac aac cat gaa tac cgg atg cag cag ctt	864

109180*EE4DE360

Gln	Arg	Ile	Ala	Leu	Ser	Asn	Asn	His	Glu	Tyr	Arg	Met	Gln	Gln	Leu		
275							280					285					
gcc	ctg	caa	agc	agc	gga	cag	gcg	ctt	cgg	gca	gca	cag	aac	agc	cgc	912	
Ala	Leu	Gln	Ser	Ser	Gly	Gln	Ala	Leu	Arg	Ala	Ala	Gln	Asn	Ser	Arg		
290						295				300							
tat	ccc	acc	gtt	tct	gcc	cat	gtc	ggc	tat	cag	aat	aac	ctc	tac	act	960	
Tyr	Pro	Thr	Val	Ser	Ala	His	Val	Gly	Tyr	Gln	Asn	Asn	Leu	Tyr	Thr		
305					310					315					320		
tca	tct	gcg	cag	aat	aat	gac	tac	cac	tat	cgg	ggc	aaa	ggg	atg	agc	1008	
Ser	Ser	Ala	Gln	Asn	Asn	Asp	Tyr	His	Tyr	Arg	Gly	Lys	Gly	Met	Ser		
				325					330					335			
gtc	ggc	gta	cag	ttg	aat	ttg	ccg	ctt	tat	acc	ggc	gga	gaa	ttg	tgc	1056	
Val	Gly	Val	Gln	Leu	Asn	Leu	Pro	Leu	Tyr	Thr	Gly	Gly	Glu	Leu	Ser		
				340				345					350				
ggc	aaa	atc	cat	gaa	gcc	gaa	gcg	caa	tac	ggg	gcc	gcc	gaa	gca	cag	1104	
Gly	Lys	Ile	His	Glu	Ala	Glu	Ala	Gln	Tyr	Gly	Ala	Ala	Glu	Ala	Gln		
	355					360					365						
ctg	acc	gca	acc	gag	cgg	cac	atc	aaa	ctc	gcc	gta	cgc	cag	gct	tat	1152	
Leu	Thr	Ala	Thr	Glu	Arg	His	Ile	Lys	Leu	Ala	Val	Arg	Gln	Ala	Tyr		
	370					375					380						
acc	gaa	agc	ggc	gcg	ggc	cgt	tac	caa	atc	atg	gcg	caa	gaa	cgg	gtr	1200	
Thr	Glu	Ser	Gly	Ala	Ala	Arg	Tyr	Gln	Ile	Met	Ala	Gln	Glu	Arg	Val		
385					390					395				400			
ttg	gaa	agc	agc	cgt	ttg	aaa	ctg	aaa	tgc	acc	gaa	acc	ggc	caa	caa	1248	
Leu	Glu	Ser	Ser	Arg	Leu	Lys	Leu	Lys	Ser	Thr	Glu	Thr	Gly	Gln	Gln		
				405				410					415				
tac	ggc	atc	cgc	aac	cgg	ctg	gaa	gta	ata	cgg	gcg	cgg	cag	gaa	gtc	1296	
Tyr	Gly	Ile	Arg	Asn	Arg	Leu	Glu	Val	Ile	Arg	Ala	Arg	Gln	Glu	Val		
			420				425						430				
gcc	caa	gca	gaa	cag	aaa	ctg	gct	caa	gca	cgg	tat	aaa	ttc	atg	ctg	1344	
Ala	Gln	Ala	Glu	Gln	Lys	Leu	Ala	Gln	Ala	Arg	Tyr	Lys	Phe	Met	Leu		
		435				440						445					
gct	tat	ttg	cgc	ttg	gtg	aaa	gag	agc	ggg	tta	ggg	ttg	gaa	acg	gta	1392	
Ala	Tyr	Leu	Arg	Leu	Val	Lys	Glu	Ser	Gly	Leu	Gly	Leu	Glu	Thr	Val		
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ttt	gcg	gaa	taa													1404	
Phe	Ala	Glu															
465																	

<210> 69
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 <212> PRT
 <213> Neisseria meningitidis

<400> 69
 Met Thr Leu Leu Asn Leu Met Ile Met Gln Asp Tyr Gly Ile Ser Val
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09830433 084604

Cys	Leu	Thr	Leu	Thr	Pro	Tyr	Leu	Gln	His	Glu	Leu	Phe	Ser	Ala	Met	20	25	30
Lys	Ser	Tyr	Phe	Ser	Lys	Tyr	Ile	Leu	Pro	Val	Ser	Leu	Phe	Thr	Leu	35	40	45
Pro	Leu	Ser	Leu	Ser	Pro	Ser	Val	Ser	Ala	Phe	Thr	Leu	Pro	Glu	Ala	50	55	60
Trp	Arg	Ala	Ala	Gln	Gln	His	Ser	Ala	Asp	Phe	Gln	Ala	Ser	His	Tyr	65	70	75
Gln	Arg	Asp	Ala	Val	Arg	Ala	Arg	Gln	Gln	Gln	Ala	Lys	Ala	Ala	Phe	85	90	95
Leu	Pro	His	Val	Ser	Ala	Asn	Ala	Ser	Tyr	Gln	Arg	Gln	Pro	Pro	Ser	100	105	110
Ile	Ser	Ser	Thr	Arg	Glu	Thr	Gln	Gly	Trp	Ser	Val	Gln	Val	Gly	Gln	115	120	125
Thr	Leu	Phe	Asp	Ala	Ala	Lys	Phe	Ala	Gln	Tyr	Arg	Gln	Ser	Arg	Phe	130	135	140
Asp	Thr	Gln	Ala	Ala	Glu	Gln	Arg	Phe	Asp	Ala	Ala	Arg	Glu	Glu	Leu	145	150	155
Leu	Leu	Lys	Val	Ala	Glu	Ser	Tyr	Phe	Asn	Val	Leu	Leu	Ser	Arg	Asp	165	170	175
Thr	Val	Ala	Ala	His	Ala	Ala	Glu	Lys	Glu	Ala	Tyr	Ala	Gln	Gln	Val	180	185	190
Arg	Gln	Ala	Gln	Ala	Leu	Phe	Asn	Lys	Gly	Ala	Ala	Thr	Ala	Leu	Asp	195	200	205
Ile	His	Glu	Ala	Lys	Ala	Gly	Tyr	Asp	Asn	Ala	Leu	Ala	Gln	Glu	Ile	210	215	220
Ala	Val	Leu	Ala	Glu	Lys	Gln	Thr	Tyr	Glu	Asn	Gln	Leu	Asn	Asp	Tyr	225	230	235
Thr	Asp	Leu	Asp	Ser	Lys	Gln	Ile	Glu	Ala	Ile	Asp	Thr	Ala	Asn	Leu	245	250	255
Leu	Ala	Arg	Tyr	Leu	Pro	Lys	Leu	Glu	Arg	Tyr	Ser	Leu	Asp	Glu	Trp	260	265	270
Gln	Arg	Ile	Ala	Leu	Ser	Asn	Asn	His	Glu	Tyr	Arg	Met	Gln	Gln	Leu	275	280	285
Ala	Leu	Gln	Ser	Ser	Gly	Gln	Ala	Leu	Arg	Ala	Ala	Gln	Asn	Ser	Arg	290	295	300
Tyr	Pro	Thr	Val	Ser	Ala	His	Val	Gly	Tyr	Gln	Asn	Asn	Leu	Tyr	Thr	305	310	315
Ser	Ser	Ala	Gln	Asn	Asn	Asp	Tyr	His	Tyr	Arg	Gly	Lys	Gly	Met	Ser	325	330	335

0930433 081601

Val Gly Val Gln Leu Asn Leu Pro Leu Tyr Thr Gly Gly Glu Leu Ser
 340 345 350

Gly Lys Ile His Glu Ala Glu Ala Gln Tyr Gly Ala Ala Glu Ala Gln
 355 360 365

Leu Thr Ala Thr Glu Arg His Ile Lys Leu Ala Val Arg Gln Ala Tyr
 370 375 380

Thr Glu Ser Gly Ala Ala Arg Tyr Gln Ile Met Ala Gln Glu Arg Val
 385 390 395 400

Leu Glu Ser Ser Arg Leu Lys Leu Lys Ser Thr Glu Thr Gly Gln Gln
 405 410 415

Tyr Gly Ile Arg Asn Arg Leu Glu Val Ile Arg Ala Arg Gln Glu Val
 420 425 430

Ala Gln Ala Glu Gln Lys Leu Ala Gln Ala Arg Tyr Lys Phe Met Leu
 435 440 445

Ala Tyr Leu Arg Leu Val Lys Glu Ser Gly Leu Gly Leu Glu Thr Val
 450 455 460

Phe Ala Glu
 465

<210> 70
 <211> 696
 <212> DNA
 <213> Neisseria gonorrhoeae

<220>
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 <222> (1)..(693)

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 Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn
 1 5 10 15

aca ttg ggc att tgc gcg att tta gcc ttt tgt ttt ggc gcg gcc atc 96
 Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
 20 25 30

gca tca ggt tat cac ttg gaa tat gaa tac gcc tac cgt tat tct gcc 144
 Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala
 35 40 45

gtg ggc gct ttg gct tgg gtt gta ttt tta tta tta ttg gca cgc gcc 192
 Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly
 50 55 60

ttc cgc cgc gtt tct tca gtt gtt tta ctg att tac gtc gcc aca acc 240
 Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr
 65 70 75 80

093043 08150


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<210> 71
<211> 231
<212> PRT
<213> Neisseria gonorrhoeae
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1				5					10					15	
Thr	Leu	Gly	Ile	Cys	Ala	Leu	Leu	Ala	Phe	Cys	Phe	Gly	Ala	Ala	Ile
			20					25					30		
Ala	Ser	Gly	Tyr	His	Leu	Glu	Tyr	Glu	Tyr	Gly	Tyr	Arg	Tyr	Ser	Ala
		35					40					45			
Val	Gly	Ala	Leu	Ala	Ser	Val	Val	Phe	Leu	Leu	Leu	Leu	Ala	Arg	Gly
	50					55					60				
Phe	Pro	Arg	Val	Ser	Ser	Val	Val	Leu	Leu	Ile	Tyr	Val	Gly	Thr	Thr

65	70	75	80
Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln			
85		90	95
Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe			
100	105		110
Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe			
115	120		125
Ile Phe Gly Leu Thr Val Trp Lys Tyr Cys Val Ser Val Gly Val Phe			
130	135		140
Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile			
145	150	155	160
Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Glu Lys Ile Ala Gly			
	165	170	175
Asp Lys Asp Trp Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe			
	180	185	190
Asp Leu Tyr Tyr Asp Leu Ala Phe Arg Ala Gly Thr Ile Cys Arg Gln			
195	200		205
Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr			
210	215		220
Pro Pro Thr Cys Ala Gln Val			
225	230		

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 <211> 2607
 <212> DNA
 <213> Neisseria meningitidis

<220>
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 <222> (1)..(2604)

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 gaa tac tac gac gcg cgt gcg gcg tgt gag ggc atc aaa ccc gcc tct 96
 Glu Tyr Tyr Asp Ala Arg Ala Ala Cys Glu Gly Ile Lys Pro Gly Ser
 20 25 30
 tac gac aag ctg cct tac acg agc cgc att ttg gcg gag aat ttg gtc 144
 Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
 35 40 45
 aac cgc gcg gac aaa gtc gat ttg ccg acg ctg caa agc tgg ctg ggt 192
 Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
 50 55 60

09830433 081604

cag ctg att gag gga aaa cag gaa atc gac ttt oct tgg tat ccg gcg Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala 65 70 75 80	240
cgg gtg gtg tgc cac gat att ctg ggg cag acc gcg ttg gtg gat ttg Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu 85 90 95	288
gca ggt ctg cgc gat gcg att gcc gaa aaa ggc ggc gat cct gcc aaa Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys 100 105 110	336
gtg aat ccg gtg gtg caa acc cag ctg atc gtc gac cac tgg ctg gcg Val Asn Pro Val Val Gln Thr Gln Leu Ile Val Asp His Ser Leu Ala 115 120 125	384
gtg gaa tgc ggc ggc tac gac ccc gat gcg ttc cgc aaa aac cgc gaa Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu 130 135 140	432
atc gaa gac aga cgt aac gaa gac cgt ttc cac ttc atc aac tgg aca Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr 145 150 155 160	480
aaa acc gct ttt gaa aat gtg gac gtg att ccg gcg ggc aac ggc atc Lys Thr Ala Phe Glu Asn Val Asp Val Ile Pro Ala Gly Asn Gly Ile 165 170 175	528
atg cac caa atc aat cta gaa aaa atg tgg ccc gtc gtc caa gtc aaa Met His Gln Ile Asn Leu Glu Lys Met Ser Pro Val Val Gln Val Lys 180 185 190	576
aac ggc gtg gct ttc ccc gat acc tgc gtc ggc acg gat tgg cac acg Asn Gly Val Ala Phe Pro Asp Thr Cys Val Gly Thr Asp Ser His Thr 195 200 205	624
cca cac gtc gat gcg ctg ggc gtg att tcc gtg ggc gtg ggc gga ttg Pro His Val Asp Ala Leu Gly Val Ile Ser Val Gly Val Gly Gly Leu 210 215 220	672
gaa gcg gaa acc gta atg ctg gga cgc gcg tcc atg atg cgc ctg ccc Glu Ala Glu Thr Val Met Leu Gly Arg Ala Ser Met Met Arg Leu Pro 225 230 235 240	720
gat att gtc ggc gtt gag ctg aac ggc aaa cgg aag gcg ggc att acg Asp Ile Val Gly Val Glu Leu Asn Gly Lys Arg Lys Ala Gly Ile Thr 245 250 255	768
gcg acg gat att gtg ttg gca ctg acc gag ttt ctg cgc aaa gaa cgc Ala Thr Asp Ile Val Leu Ala Leu Thr Glu Phe Leu Arg Lys Glu Arg 260 265 270	816
gtg gtc ggg gcg ttt gtc gaa ttc ttc ggc gag ggc gcg aga agc ctg Val Val Gly Ala Phe Val Glu Phe Phe Gly Glu Gly Ala Arg Ser Leu 275 280 285	864
tct atc ggc gac cgc gcg acc att tcc aac atg acg ccg gag ttc ggc Ser Ile Gly Asp Arg Ala Thr Ile Ser Asn Met Thr Pro Glu Phe Gly 290 295 300	912

09030433 081601

gcg act gcc gcg atg ttc gct att gat gag caa acc att gat tat ttg	960
Ala Thr Ala Ala Met Phe Ala Ile Asp Glu Gln Thr Ile Asp Tyr Leu	
305 310 315 320	
aaa ctg acc gga cgc gac gac gcg cag gtg aaa ttg gtg gaa acc tac	1008
Lys Leu Thr Gly Arg Asp Asp Ala Gln Val Lys Leu Val Glu Thr Tyr	
325 330 335	
gcc aaa acc gca ggc ttg tgg gca gat gcc ttg aaa acc gcc gtt tat	1056
Ala Lys Thr Ala Gly Leu Trp Ala Asp Ala Leu Lys Thr Ala Val Tyr	
340 345 350	
ccg cgc gtt ttg aaa ttt gat ttg agc agc gta acg cgc aat atg gca	1104
Pro Arg Val Leu Lys Phe Asp Leu Ser Ser Val Thr Arg Asn Met Ala	
355 360 365	
ggc ccg agc aac ccg cac gcg cgt ttt gcg acc gcc gat ttg gcc ggc	1152
Gly Pro Ser Asn Pro His Ala Arg Phe Ala Thr Ala Asp Leu Ala Gly	
370 375 380	
aaa ggc ttg gct aaa cct tac gaa gag cct tca gac ggc caa atg cct	1200
Lys Gly Leu Ala Lys Pro Tyr Glu Glu Pro Ser Asp Gly Gln Met Pro	
385 390 395 400	
gac ggt gca gtg att att gcc gcg att act tcc tgt acc aat act tcc	1248
Asp Gly Ala Val Ile Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser	
405 410 415	
aat ccg cgc aac gtt gtc gcc gcc gcg ctg ttg gca cgc aat gcc aac	1296
Asn Pro Arg Asn Val Val Ala Ala Ala Leu Leu Ala Arg Asn Ala Asn	
420 425 430	
cgc ctc ggc ttg caa cgc aaa cct tgg gtg aaa cct tcc ttg gcc ccg	1344
Arg Leu Gly Leu Gln Arg Lys Pro Trp Val Lys Ser Ser Phe Ala Pro	
435 440 445	
ggt tca aaa gta gcc gaa atc tat ttg aaa gaa gca gat ctg ctg ccc	1392
Gly Ser Lys Val Ala Glu Ile Tyr Leu Lys Glu Ala Asp Leu Leu Pro	
450 455 460	
gaa atg gaa aaa ctc ggc ttc ggt atc gtt gcc ttc gca tgt acc acc	1440
Glu Met Glu Lys Leu Gly Phe Gly Ile Val Ala Phe Ala Cys Thr Thr	
465 470 475 480	
tgt aac ggc atg agc ggc gcg ctg gat ccg aaa atc cag aaa gaa atc	1488
Cys Asn Gly Met Ser Gly Ala Leu Asp Pro Lys Ile Gln Lys Glu Ile	
485 490 495	
atc gac cgc gat ttg tac gcc acc gcc gta ttg tca ggc aac cgc aac	1536
Ile Asp Arg Asp Leu Tyr Ala Thr Ala Val Leu Ser Gly Asn Arg Asn	
500 505 510	
ttt gac ggc cgt atc cat ccg tat gcg aaa cag gct ttc ctc gct tcg	1584
Phe Asp Gly Arg Ile His Pro Tyr Ala Lys Gln Ala Phe Leu Ala Ser	
515 520 525	
cct ccg ttg gtc gtt gcc tac gcg ctg gca ggc agc atc cgt ttc gat	1632
Pro Pro Leu Val Val Ala Tyr Ala Leu Ala Gly Ser Ile Arg Phe Asp	
530 535 540	

tatt ile 545	gaa Glu	aac Asn	gac Asp	gta Val	ctc Leu	ggc Gly	gtt Val	gca Ala	gac Asp	ggc Gly	aaa Lys	gaa Glu	atc Ile	cgc Arg	ctg Leu	1680
aaa Lys	gac Asp	att Ile	tgg Trp	cct Pro	acc Thr	gat Asp	gaa Glu	gaa Glu	atc Ile	gat Asp	gcc Ala	atc Ile	gtt Val	gcc Ala	gaa Glu	1728
tat Tyr	gtg Val	aaa Lys	ccg Pro	cag Gln	caa Gln	ttt Phe	cgc Arg	gac Asp	gtt Val	tat Tyr	atc Ile	ccg Pro	atg Met	ttc Phe	gac Asp	1776
acc Thr	ggc Gly	aca Thr	gcg Ala	caa Gln	aaa Lys	gca Ala	cca Pro	agc Ser	ccg Pro	ctg Leu	tac Tyr	gac Asp	tgg Trp	cgt Arg	cca Pro	1824
atg Met	tct Ser	acc Thr	tat Tyr	atc Ile	cgc Arg	cgc Arg	cca Pro	cct Pro	tac Tyr	tgg Trp	gaa Glu	ggc Gly	gca Ala	ctg Leu	gca Ala	1872
ggg Gly	gaa Glu	cgc Arg	aca Thr	tta Leu	agc Ser	ggc Gly	atg Met	cgt Arg	ccg Pro	ctg Leu	gcg Ala	att Ile	ttg Leu	ccc Pro	gac Asp	1920
aac Asn	atc Ile	acc Thr	acc Thr	gac Asp	cat His	ctc Leu	tgc Ser	cca Pro	tcc Ser	aat Asn	gcg Ala	att Ile	ttg Leu	gca Ala	agc Ser	1968
agt Ser	gcc Ala	gca Ala	ggc Gly	gaa Glu	tat Tyr	ttg Leu	gca Ala	aaa Lys	atg Met	ggc Gly	ttg Leu	cct Pro	gaa Glu	gaa Glu	gac Asp	2016
ttc Phe	aac Asn	tct Ser	tac Tyr	gca Ala	acc Thr	cac His	cgt Arg	ggc Gly	gac Asp	cac His	ttg Leu	acc Thr	gcc Ala	caa Gln	cgc Arg	2064
gca Ala	acc Thr	ttc Phe	gcc Ala	aat Asn	ccg Pro	aaa Lys	ctg Leu	ttt Phe	aac Asn	gaa Glu	atg Met	gtg Val	aga Arg	aac Asn	gaa Glu	2112
gac Asp	ggc Gly	agc Ser	gta Val	cgc Arg	caa Gln	ggc Gly	tgc Ser	ctg Leu	gca Ala	cgc Arg	gtt Val	gaa Glu	ccc Pro	gaa Glu	ggc Gly	2160
caa Gln	acc Thr	atg Met	cgc Arg	atg Met	tgg Trp	gaa Glu	gcc Ala	atc Ile	gaa Glu	acc Thr	tat Tyr	atg Met	aac Asn	cgc Arg	aaa Lys	2208
cag Gln	ccg Pro	ctc Leu	atc Ile	atc Ile	att Ile	gcc Ala	ggc Gly	gcg Ala	gac Asp	tac Tyr	ggc Gly	caa Gln	ggc Gly	tca Ser	agc Ser	2256
cgc Arg	gac Asp	tgg Trp	gct Ala	gca Ala	aaa Lys	ggc Gly	gta Val	cgc Arg	ctc Leu	gcc Ala	ggc Gly	gtg Val	gaa Glu	gcg Ala	att Ile	2304
gtt Val	gcc Ala	gaa Glu	ggc Gly	ttc Phe	gag Glu	cgt Arg	atc Ile	cac His	cgc Arg	acc Thr	aac Asn	ttg Leu	atc Ile	ggc Gly	atg Met	2352

tat gtg aaa ccg cag caa ttt cgc gac gtt tat atc ccg atg ttc gac 1776
Tyr Val Lys Pro Gln Gln Phe Arg Asp Val Tyr Ile Pro Met Phe Asp
580 585 590

atg tct acc tat atc cgc cgc cca cct tac tgg gaa ggc gca ctg gca 1872
Met Ser Thr Tyr Ile Arg Arg Pro Pro Tyr Trp Glu Gly Ala Leu Ala
610 615 620

aac atc acc acc gac cat ctc tog cca tcc aat gcg att ttg gca agc 1968
Asn Ile Thr Thr Asp His Leu Ser Pro Ser Asn Ala Ile Leu Ala Ser
645 650 655

ttc aac tct tac gca acc cac cgt ggc gac cac ttg acc gcc caa cgc 2064
Phe Asn Ser Tyr Ala Thr His Arg Gly Asp His Leu Thr Ala Gln Arg
675 680 685

gac ggc agc gta cgc caa ggt tcg ctg gca cgc gtt gaa ccc gaa ggc 2160
Asp Gly Ser Val Arg Gln Gly Ser Leu Ala Arg Val Glu Pro Glu Gly
705 710 715 720

cag ccg ctc atc atc att gcc ggc gcg gac tac ggt caa ggc tca agc 2256
Gln Pro Leu Ile Ile Ile Ala Gly Ala Asp Tyr Gly Gln Gly Ser ser
740 745 750

gtt gcc gaa ggc ttc gag cgt atc cac cgc acc aac ttg atc ggt atg 2352
Val Ala Glu Gly Phe Glu Arg Ile His Arg Thr Asn Leu Ile Gly Met
770 775 780

ggc gtg ttg ccg ctg cag ttc aaa ccg ggt acc aac cgc cac acc ctg 2400
 Gly Val Leu Pro Leu Gln Phe Lys Pro Gly Thr Asn Arg His Thr Leu
 785 790 795 800

caa ctg gac ggt acg gaa acc tac gac gtt gtc ggc gaa cgc aca ccg 2448
 Gln Leu Asp Gly Thr Glu Thr Tyr Asp Val Val Gly Glu Arg Thr Pro
 805 810 815

cgc tgc gac ctg acc ctt gtg att cac cgt aaa aac ggc gag acc gtc 2496
 Arg Cys Asp Leu Thr Leu Val Ile His Arg Lys Asn Gly Glu Thr Val
 820 825 830

gaa gtc ccc att acc tgc cgc ctc gat acc gca gaa gaa gtg ttg gta 2544
 Glu Val Pro Ile Thr Cys Arg Leu Asp Thr Ala Glu Glu Val Leu Val
 835 840 845

tat gaa gcc ggt ggc gta ttg caa cgg ttt gca cag gat ttt ttg gaa 2592
 Tyr Glu Ala Gly Gly Val Leu Gln Arg Phe Ala Gln Asp Phe Leu Glu
 850 855 860

ggg aac gcg gct tag 2607
 Gly Asn Ala Ala
 865

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 <213> Neisseria meningitidis

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 20 25 30

Tyr Asp Lys Leu Pro Tyr Thr Ser Arg Ile Leu Ala Glu Asn Leu Val
 35 40 45

Asn Arg Ala Asp Lys Val Asp Leu Pro Thr Leu Gln Ser Trp Leu Gly
 50 55 60

Gln Leu Ile Glu Gly Lys Gln Glu Ile Asp Phe Pro Trp Tyr Pro Ala
 65 70 75 80

Arg Val Val Cys His Asp Ile Leu Gly Gln Thr Ala Leu Val Asp Leu
 85 90 95

Ala Gly Leu Arg Asp Ala Ile Ala Glu Lys Gly Gly Asp Pro Ala Lys
 100 105 110

Val Asn Pro Val Val Gln Thr Gln Leu Ile Val Asp His Ser Leu Ala
 115 120 125

Val Glu Cys Gly Gly Tyr Asp Pro Asp Ala Phe Arg Lys Asn Arg Glu
 130 135 140

Ile Glu Asp Arg Arg Asn Glu Asp Arg Phe His Phe Ile Asn Trp Thr
 145 150 155 160

09030437 081601
 T037037 004000000

Lys	Thr	Ala	Phe	Glu	Asn	Val	Asp	Val	Ile	Pro	Ala	Gly	Asn	Gly	Ile	165	170	175
Met	His	Gln	Ile	Asn	Leu	Glu	Lys	Met	Ser	Pro	Val	Val	Gln	Val	Lys	180	185	190
Asn	Gly	Val	Ala	Phe	Pro	Asp	Thr	Cys	Val	Gly	Thr	Asp	Ser	His	Thr	195	200	205
Pro	His	Val	Asp	Ala	Leu	Gly	Val	Ile	Ser	Val	Gly	Val	Gly	Gly	Leu	210	215	220
Glu	Ala	Glu	Thr	Val	Met	Leu	Gly	Arg	Ala	Ser	Met	Met	Arg	Leu	Pro	225	230	235
Asp	Ile	Val	Gly	Val	Glu	Leu	Asn	Gly	Lys	Arg	Lys	Ala	Gly	Ile	Thr	245	250	255
Ala	Thr	Asp	Ile	Val	Leu	Ala	Leu	Thr	Glu	Phe	Leu	Arg	Lys	Glu	Arg	260	265	270
Val	Val	Gly	Ala	Phe	Val	Glu	Phe	Phe	Gly	Glu	Gly	Ala	Arg	Ser	Leu	275	280	285
Ser	Ile	Gly	Asp	Arg	Ala	Thr	Ile	Ser	Asn	Met	Thr	Pro	Glu	Phe	Gly	290	295	300
Ala	Thr	Ala	Ala	Met	Phe	Ala	Ile	Asp	Glu	Gln	Thr	Ile	Asp	Tyr	Leu	305	310	315
Lys	Leu	Thr	Gly	Arg	Asp	Asp	Ala	Gln	Val	Lys	Leu	Val	Glu	Thr	Tyr	325	330	335
Ala	Lys	Thr	Ala	Gly	Leu	Trp	Ala	Asp	Ala	Leu	Lys	Thr	Ala	Val	Tyr	340	345	350
Pro	Arg	Val	Leu	Lys	Phe	Asp	Leu	Ser	Ser	Val	Thr	Arg	Asn	Met	Ala	355	360	365
Gly	Pro	Ser	Asn	Pro	His	Ala	Arg	Phe	Ala	Thr	Ala	Asp	Leu	Ala	Gly	370	375	380
Lys	Gly	Leu	Ala	Lys	Pro	Tyr	Glu	Glu	Pro	Ser	Asp	Gly	Gln	Met	Pro	385	390	395
Asp	Gly	Ala	Val	Ile	Ile	Ala	Ala	Ile	Thr	Ser	Cys	Thr	Asn	Thr	Ser	405	410	415
Asn	Pro	Arg	Asn	Val	Val	Ala	Ala	Ala	Leu	Leu	Ala	Arg	Asn	Ala	Asn	420	425	430
Arg	Leu	Gly	Leu	Gln	Arg	Lys	Pro	Trp	Val	Lys	Ser	Ser	Phe	Ala	Pro	435	440	445
Gly	Ser	Lys	Val	Ala	Glu	Ile	Tyr	Leu	Lys	Glu	Ala	Asp	Leu	Leu	Pro	450	455	460
Glu	Met	Glu	Lys	Leu	Gly	Phe	Gly	Ile	Val	Ala	Phe	Ala	Cys	Thr	Thr	465	470	475

Cys	Asn	Gly	Met	Ser	Gly	Ala	Leu	Asp	Pro	Lys	Ile	Gln	Lys	Glu	Ile	485	490	495
Ile	Asp	Arg	Asp	Leu	Tyr	Ala	Thr	Ala	Val	Leu	Ser	Gly	Asn	Arg	Asn	500	505	510
Phe	Asp	Gly	Arg	Ile	His	Pro	Tyr	Ala	Lys	Gln	Ala	Phe	Leu	Ala	Ser	515	520	525
Pro	Pro	Leu	Val	Val	Ala	Tyr	Ala	Leu	Ala	Gly	Ser	Ile	Arg	Phe	Asp	530	535	540
Ile	Glu	Asn	Asp	Val	Leu	Gly	Val	Ala	Asp	Gly	Lys	Glu	Ile	Arg	Leu	545	550	555
Lys	Asp	Ile	Trp	Pro	Thr	Asp	Glu	Glu	Ile	Asp	Ala	Ile	Val	Ala	Glu	565	570	575
Tyr	Val	Lys	Pro	Gln	Gln	Phe	Arg	Asp	Val	Tyr	Ile	Pro	Met	Phe	Asp	580	585	590
Thr	Gly	Thr	Ala	Gln	Lys	Ala	Pro	Ser	Pro	Leu	Tyr	Asp	Trp	Arg	Pro	595	600	605
Met	Ser	Thr	Tyr	Ile	Arg	Arg	Pro	Pro	Tyr	Trp	Glu	Gly	Ala	Leu	Ala	610	615	620
Gly	Glu	Arg	Thr	Leu	Ser	Gly	Met	Arg	Pro	Leu	Ala	Ile	Leu	Pro	Asp	625	630	635
Asn	Ile	Thr	Thr	Asp	His	Leu	Ser	Pro	Ser	Asn	Ala	Ile	Leu	Ala	Ser	645	650	655
Ser	Ala	Ala	Gly	Glu	Tyr	Leu	Ala	Lys	Met	Gly	Leu	Pro	Glu	Glu	Asp	660	665	670
Phe	Asn	Ser	Tyr	Ala	Thr	His	Arg	Gly	Asp	His	Leu	Thr	Ala	Gln	Arg	675	680	685
Ala	Thr	Phe	Ala	Asn	Pro	Lys	Leu	Phe	Asn	Glu	Met	Val	Arg	Asn	Glu	690	695	700
Asp	Gly	Ser	Val	Arg	Gln	Gly	Ser	Leu	Ala	Arg	Val	Glu	Pro	Glu	Gly	705	710	715
Gln	Thr	Met	Arg	Met	Trp	Glu	Ala	Ile	Glu	Thr	Tyr	Met	Asn	Arg	Lys	725	730	735
Gln	Pro	Leu	Ile	Ile	Ile	Ala	Gly	Ala	Asp	Tyr	Gly	Gln	Gly	Ser	Ser	740	745	750
Arg	Asp	Trp	Ala	Ala	Lys	Gly	Val	Arg	Leu	Ala	Gly	Val	Glu	Ala	Ile	755	760	765
Val	Ala	Glu	Gly	Phe	Glu	Arg	Ile	His	Arg	Thr	Asn	Leu	Ile	Gly	Met	770	775	780
Gly	Val	Leu	Pro	Leu	Gln	Phe	Lys	Pro	Gly	Thr	Asn	Arg	His	Thr	Leu	785	790	795

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<212> DNA
<213> Neisseria meningitidis

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<221> CDS
<222> (1)..(1167)
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Met	Pro	Gln	Ile	Lys	Ile	Pro	Ala	Val	Tyr	Tyr	Arg	Gly	Gly	Thr	Ser	
1				5					10					15		
aaa	ggc	gtg	ttt	ttc	aaa	cgt	tcc	gac	ctg	ccc	gag	gcg	gcg	cgg	gaa	96
Lys	Gly	Val	Phe	Phe	Lys	Arg	Ser	Asp	Leu	Pro	Glu	Ala	Ala	Arg	Glu	
			20					25					30			
gcg	gga	agc	gca	cgc	gac	aaa	atc	ctc	ttg	cgc	gta	ctc	ggc	agc	ccg	144
Ala	Gly	Ser	Ala	Arg	Asp	Lys	Ile	Leu	Leu	Arg	Val	Leu	Gly	Ser	Pro	
			35				40					45				
gat	ccc	tac	ggc	aag	cag	ata	gac	ggg	ttg	ggc	aac	gcc	agc	tcg	tcc	192
Asp	Pro	Tyr	Gly	Lys	Gln	Ile	Asp	Gly	Leu	Gly	Asn	Ala	Ser	Ser	Ser	
	50					55					60					
acc	agc	aag	gcg	gtg	att	ttg	gac	aag	tcc	gaa	cgc	gcc	gat	cac	gat	240
Thr	Ser	Lys	Ala	Val	Ile	Leu	Asp	Lys	Ser	Glu	Arg	Ala	Asp	His	Asp	
65					70					75				80		
gtc	gat	tac	ctt	ttc	ggg	caa	gtt	tcc	atc	gac	aaa	cct	ttt	gtc	gat	288
Val	Asp	Tyr	Leu	Phe	Gly	Gln	Val	Ser	Ile	Asp	Lys	Pro	Phe	Val	Asp	
				85					90				95			
tgg	agt	ggc	aac	tgc	ggc	aac	ctc	acc	gcc	gcc	gtg	ggc	gca	ttt	gcc	336
Trp	Ser	Gly	Asn	Cys	Gly	Asn	Leu	Thr	Ala	Ala	Val	Gly	Ala	Phe	Ala	
			100					105				110				
atc	gag	caa	ggc	ttg	gtc	gat	aaa	ggc	aag	att	cct	tca	gac	ggc	atc	384
Ile	Glu	Gln	Gly	Leu	Val	Asp	Lys	Gly	Lys	Ile	Pro	Ser	Asp	Gly	Ile	
		115					120					125				

tgc Cys	aca Thr	gtc Val	aaa Lys	atc Ile	tgg Trp	cag Gln	aaa Lys	aac Asn	atc Ile	ggc Gly	aaa Lys	acc Thr	att Ile	att Ile	gcc Ala	432
130135140																
cat His	gta Val	cgg Pro	atg Met	caa Gln	aac Asn	ggc Gly	gca Ala	gtt Val	ttg Leu	gaa Glu	aca Thr	ggc Gly	gat Asp	ttt Phe	gag Glu	480
145150155160																
ctc Leu	gac Asp	ggc Gly	gta Val	acg Thr	ttc Phe	cgg Pro	gca Ala	gcc Ala	gaa Glu	gta Val	caa Gln	atc Ile	gaa Glu	ttt Phe	ctt Leu	528
165170175																
gat Asp	cca Pro	gcc Ala	gac Asp	ggc Gly	gaa Glu	ggc Gly	agt Ser	atg Met	ttc Phe	cca Pro	acc Thr	ggc Gly	aat Asn	ttg Leu	gtc Val	576
180185190																
gat Asp	gaa Glu	att Ile	gat Asp	gtg Val	cgg Pro	aat Asn	ata Ile	ggc Gly	cgt Arg	ttg Leu	aaa Lys	gcc Ala	acg Thr	ctc Leu	atc Ile	624
195200205																
aac Asn	gcg Ala	ggc Gly	att Ile	cgg Pro	acc Thr	gtt Val	ttc Phe	ctg Leu	aat Asn	gcc Ala	gcc Ala	gac Asp	ttg Leu	ggc Gly	tac Tyr	672
210215220																
acg Thr	ggc Gly	aaa Lys	gag Glu	ttg Leu	caa Gln	gac Asp	gac Asp	atc Ile	aac Asn	aac Asn	gat Asp	gcc Ala	gca Ala	gct Ala	ttg Leu	720
225230235240																
gaa Glu	aaa Lys	ttc Phe	gag Glu	aaa Lys	atc Ile	cgc Arg	gct Ala	tac Tyr	ggc Gly	ctg Ala	ctg Leu	aaa Lys	atg Met	ggc Gly	ctg Leu	768
245250255																
atc Ile	agc Ser	gac Asp	gta Val	tcc Ser	gaa Glu	gct Ala	gcc Ala	gcc Ala	cgc Arg	gcg Ala	cac His	acg Thr	ccg Pro	aaa Lys	gtc Val	816
260265270																
gcc Ala	ttc Phe	gtc Val	gcg Ala	ccc Pro	gcc Ala	gcc Ala	gat Asp	tac Tyr	acc Thr	gcc Ala	tcc Ser	agt Ser	ggc Gly	aaa Lys	acc Thr	864
275280285																
gtg Val	aat Asn	gcc Ala	gcc Ala	gac Asp	atc Ile	gat Asp	ttg Leu	ctg Leu	gta Val	cgc Arg	gcc Ala	ctg Leu	agc Ser	atg Met	ggc Gly	912
290295300																
aaa Lys	ttg Leu	cac His	cac His	gcg Ala	atg Met	atg Met	ggc Gly	acc Thr	gcc Ala	tct Ser	gtt Val	gcc Ala	att Ile	gcg Ala	acc Thr	960
305310315320																
gcc Ala	gcc Ala	gcc Ala	gtg Val	ccc Pro	ggc Gly	acg Thr	ctg Leu	gtc Val	aac Asn	ctt Leu	gcc Ala	gca Ala	ggc Gly	ggc Gly	gga Gly	1008
325330335																
acg Thr	cgt Arg	aaa Lys	gaa Glu	gtg Val	cgc Arg	ttc Phe	ggg Gly	cat His	cct Pro	tcc Ser	ggc Gly	aca Thr	ttg Leu	cgc Arg	gtc Val	1056
340345350																
ggc Gly	gca Ala	gcc Ala	gcc Ala	gaa Glu	tgt Cys	cag Gln	gac Asp	gga Gly	caa Gln	tgg Trp	acg Thr	gcc Ala	acc Thr	aaa Lys	gcg Ala	1104
355360365																
gtt Val	atg Met	agc Ser	cgc Arg	agc Ser	gca Ala	cgc Arg	gtg Val	atg Met	atg Met	gaa Glu	ggc Gly	tgg Trp	gtc Val	agg Arg	gtg Val	1152
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ccg Pro	gaa Glu	gat Asp	tgt Cys	ttt Phe	taa											1170
385																

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 <213> Neisseria meningitidis

<400> 75

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Lys Gly Val Phe Phe Lys Arg Ser Asp Leu Pro Glu Ala Ala Arg Glu
 20 25 30

Ala Gly Ser Ala Arg Asp Lys Ile Leu Leu Arg Val Leu Gly Ser Pro
 35 40 45

Asp Pro Tyr Gly Lys Gln Ile Asp Gly Leu Gly Asn Ala Ser Ser Ser
 50 55 60

Thr Ser Lys Ala Val Ile Leu Asp Lys Ser Glu Arg Ala Asp His Asp
 65 70 75 80

Val Asp Tyr Leu Phe Gly Gln Val Ser Ile Asp Lys Pro Phe Val Asp
 85 90 95

Trp Ser Gly Asn Cys Gly Asn Leu Thr Ala Ala Val Gly Ala Phe Ala
 100 105 110

Ile Glu Gln Gly Leu Val Asp Lys Gly Lys Ile Pro Ser Asp Gly Ile
 115 120 125

Cys Thr Val Lys Ile Trp Gln Lys Asn Ile Gly Lys Thr Ile Ile Ala
 130 135 140

His Val Pro Met Gln Asn Gly Ala Val Leu Glu Thr Gly Asp Phe Glu
 145 150 155 160

Leu Asp Gly Val Thr Phe Pro Ala Ala Glu Val Gln Ile Glu Phe Leu
 165 170 175

Asp Pro Ala Asp Gly Glu Gly Ser Met Phe Pro Thr Gly Asn Leu Val
 180 185 190

Asp Glu Ile Asp Val Pro Asn Ile Gly Arg Leu Lys Ala Thr Leu Ile
 195 200 205

Asn Ala Gly Ile Pro Thr Val Phe Leu Asn Ala Ala Asp Leu Gly Tyr
 210 215 220

Thr Gly Lys Glu Leu Gln Asp Asp Ile Asn Asn Asp Ala Ala Ala Leu
 225 230 235 240

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Glu Lys Phe Glu Lys Ile Arg Ala Tyr Gly Ala Leu Lys Met Gly Leu
 245 250 255

Ile Ser Asp Val Ser Glu Ala Ala Ala Arg Ala His Thr Pro Lys Val
 260 265 270

Ala Phe Val Ala Pro Ala Ala Asp Tyr Thr Ala Ser Ser Gly Lys Thr
 275 280 285

Val Asn Ala Ala Asp Ile Asp Leu Leu Val Arg Ala Leu Ser Met Gly
 290 295 300

Lys Leu His His Ala Met Met Gly Thr Ala Ser Val Ala Ile Ala Thr
 305 310 315 320

Ala Ala Ala Val Pro Gly Thr Leu Val Asn Leu Ala Ala Gly Gly Gly
 325 330 335

Thr Arg Lys Glu Val Arg Phe Gly His Pro Ser Gly Thr Leu Arg Val
 340 345 350

Gly Ala Ala Ala Glu Cys Gln Asp Gly Gln Trp Thr Ala Thr Lys Ala
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Val Met Ser Arg Ser Ala Arg Val Met Met Glu Gly Trp Val Arg Val
 370 375 380

Pro Glu Asp Cys Phe
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 <213> Neisseria gonorrhoeae

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ttc gcc tct ggc ttc tgc gcc ctg att tac cag gtc agc tgg cag agg 96
 Phe Ala Ser Gly Phe Cys Ala Leu Ile Tyr Gln Val Ser Trp Gln Arg
 20 25 30

ctt cta ttc agc cac ata ggt atc gat ttg agt tcg att act gtc att 144
 Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile
 35 40 45

att tct gta ttt atg gtc ggc ttg ggt gta ggt gcg tat ttc ggc gga 192
 Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly
 50 55 60

cgc att gct gac cgt ttt cct tca agt atc atc ccc ctg ttt tgc atc 240
 Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile

09030433 081500

65	70	75	80	
gct gaa gta tcc atc ggt ctg ttc ggt ttg gta agc aag ggt ctg att				288
Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Lys Gly Leu Ile	85	90	95	
tcc ggc ttg ggg cat ctt tta gtt gag gct gat ttg ccc atc atc gct				336
Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala	100	105	110	
gct gcc aat ttc ctc tta ttg ctg ctt cct acc ttt atg atg ggc gcg				384
Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala	115	120	125	
acc ttg ccc ttg ctg acc tgt ttt ttt aac cgg aaa ata cat aat gtt				432
Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val	130	135	140	
ggc gag tct atc ggt acc tta tat ttt ttc aac act ttg ggt gcg gca				480
Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala	145	150	155	160
ctc gga tcg ctt gcc gcc gcc gaa ttt ttc tac gtc ttt ttt acc ctc				528
Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu	165	170	175	
tcc caa acc att gcg ctg aca gcc tgc ctt aac ctt ctg att gct gct				576
Ser Gln Thr Ile Ala Leu Thr Ala Cys Leu Asn Leu Leu Ile Ala Ala	180	185	190	
tca gta tgc tgc gtt aca gaa agg atg gat atg gtg aac act aaa ccg				624
Ser Val Cys Cys Val Thr Glu Arg Met Asp Met Val Asn Thr Lys Pro	195	200	205	
aat act agt gtg att aat atg ctt tct ttc ctt acc gga tta ttg agc				672
Asn Thr Ser Val Ile Asn Met Leu Ser Phe Leu Thr Gly Leu Leu Ser	210	215	220	
ttg ggt ata gaa gtc ttg tgg gta agg atg ttt tcg ttc gca gca cag				720
Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln	225	230	235	240
tcc gtg cct cag gca ttt tca ttt att ctt gcc tgt ttt ctg acc ggt				768
Ser Val Pro Gln Ala Phe Ser Phe Ile Leu Ala Cys Phe Leu Thr Gly	245	250	255	
atc gcc gtc ggc gcg tat ttt ggc aaa cgg att tgc cgc agc cgc ttt				816
Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe	260	265	270	
gtt gat att ccc ttt atc ggg cag tgc ttc ttg tgg gcg ggt att gcc				864
Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala	275	280	285	
gat ttt ttg att ttg ggt gct gcg tgg ttg ttg acg ggt ttt tcc ggt				912
Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly	290	295	300	
ttc gtc cac cac gcc ggt att ttc att acc ctg tct gcc gtc gtc agg				960
Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg				

09830433 081601

305	310	315	320	
ggg ttg att ttc cca ctt gta cac cat gtg ggt acg gat ggc aac aaa				1008
Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys	325	330	335	
tcc gga cga cag gtt tcc aat gtt tat ttc gcc aac gtt gcc ggc agt				1056
Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser	340	345	350	
gca ttg ggt ccg gtc ctt atc ggc ttt gtg ata ctt gat ttg ttg tcc				1104
Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Leu Leu Ser	355	360	365	
acc caa cag att tac ctg ctc atc tgt ttg att tct gct gct gtc cct				1152
Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro	370	375	380	
ttg ttt tgt aca ctg ttc caa aaa agt ctc cga ctg aat gca gtg tcg				1200
Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser	385	390	400	
gta gca gtt tcc cta atg ttc ggc atc ctc atg ttc cta ctg ccg gat				1248
Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp	405	410	415	
tct gtc ttt caa aat att gct ggc cgt ccg gat agg ttg att gaa aac				1296
Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn	420	425	430	
aaa cac ggc att gtt gcg gtt tac cat aga gat ggt gat aag gtt gtt				1344
Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val	435	440	445	
tat ggg gcg aat gta tac gac ggc gca tac aat acc gat ata ttc aat				1392
Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn	450	455	460	
agt gtc aac ggc atc gaa cgt gcc tat ctg cta ccc tcc ctg aag tcc				1440
Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser	465	470	480	
ggc ata cgc cgc att ttc gtc gtt gga ttg agt aca ggt tcg tgg gcg				1488
Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala	485	490	495	
cgc gtc ttg tct gcc att ccg gaa atg cag tcg atg atc gtt gcg gaa				1536
Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu	500	505	510	
atc aat ccg gca tac cgt agc ctt atc gcg gac gag ccg caa atc gca				1584
Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala	515	520	525	
ccg ctt ttg cag gac aaa cgt gtt gaa att gta ttg gat gac ggt agg				1632
Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg	530	535	540	
aaa tgg ctg cgt cgc cat cct gat gaa aaa ttc gac ctg att ttg atg				1680
Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met				

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<211> 697
<212> PRT
<213> Neisseria gonorrhoeae
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      20                               25                      30

Leu Leu Phe Ser His Ile Gly Ile Asp Leu Ser Ser Ile Thr Val Ile
  35                               40                      45

Ile Ser Val Phe Met Val Gly Leu Gly Val Gly Ala Tyr Phe Gly Gly
  50                               55                      60

Arg Ile Ala Asp Arg Phe Pro Ser Ser Ile Ile Pro Leu Phe Cys Ile
  65                               70                      75                      80

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Ala Glu Val Ser Ile Gly Leu Phe Gly Leu Val Ser Lys Gly Leu Ile
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Ser Gly Leu Gly His Leu Leu Val Glu Ala Asp Leu Pro Ile Ile Ala
100 105 110

Ala Ala Asn Phe Leu Leu Leu Leu Leu Pro Thr Phe Met Met Gly Ala
115 120 125

Thr Leu Pro Leu Leu Thr Cys Phe Phe Asn Arg Lys Ile His Asn Val
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Gly Glu Ser Ile Gly Thr Leu Tyr Phe Phe Asn Thr Leu Gly Ala Ala
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Leu Gly Ser Leu Ala Ala Ala Glu Phe Phe Tyr Val Phe Phe Thr Leu
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Ser Gln Thr Ile Ala Leu Thr Ala Cys Leu Asn Leu Leu Ile Ala Ala
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Ser Val Cys Cys Val Thr Glu Arg Met Asp Met Val Asn Thr Lys Pro
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Asn Thr Ser Val Ile Asn Met Leu Ser Phe Leu Thr Gly Leu Leu Ser
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Leu Gly Ile Glu Val Leu Trp Val Arg Met Phe Ser Phe Ala Ala Gln
225 230 235 240

Ser Val Pro Gln Ala Phe Ser Phe Ile Leu Ala Cys Phe Leu Thr Gly
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Ile Ala Val Gly Ala Tyr Phe Gly Lys Arg Ile Cys Arg Ser Arg Phe
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Val Asp Ile Pro Phe Ile Gly Gln Cys Phe Leu Trp Ala Gly Ile Ala
275 280 285

Asp Phe Leu Ile Leu Gly Ala Ala Trp Leu Leu Thr Gly Phe Ser Gly
290 295 300

Phe Val His His Ala Gly Ile Phe Ile Thr Leu Ser Ala Val Val Arg
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Gly Leu Ile Phe Pro Leu Val His His Val Gly Thr Asp Gly Asn Lys
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Ser Gly Arg Gln Val Ser Asn Val Tyr Phe Ala Asn Val Ala Gly Ser
340 345 350

Ala Leu Gly Pro Val Leu Ile Gly Phe Val Ile Leu Asp Leu Leu Ser
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Thr Gln Gln Ile Tyr Leu Leu Ile Cys Leu Ile Ser Ala Ala Val Pro
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Leu Phe Cys Thr Leu Phe Gln Lys Ser Leu Arg Leu Asn Ala Val Ser
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00830433 081634

Val Ala Val Ser Leu Met Phe Gly Ile Leu Met Phe Leu Leu Pro Asp
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Ser Val Phe Gln Asn Ile Ala Gly Arg Pro Asp Arg Leu Ile Glu Asn
420 425 430

Lys His Gly Ile Val Ala Val Tyr His Arg Asp Gly Asp Lys Val Val
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Tyr Gly Ala Asn Val Tyr Asp Gly Ala Tyr Asn Thr Asp Ile Phe Asn
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Ser Val Asn Gly Ile Glu Arg Ala Tyr Leu Leu Pro Ser Leu Lys Ser
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Gly Ile Arg Arg Ile Phe Val Val Gly Leu Ser Thr Gly Ser Trp Ala
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Arg Val Leu Ser Ala Ile Pro Glu Met Gln Ser Met Ile Val Ala Glu
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Ile Asn Pro Ala Tyr Arg Ser Leu Ile Ala Asp Glu Pro Gln Ile Ala
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Pro Leu Leu Gln Asp Lys Arg Val Glu Ile Val Leu Asp Asp Gly Arg
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Lys Trp Leu Arg Arg His Pro Asp Glu Lys Phe Asp Leu Ile Leu Met
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Asn Ser Thr Trp Tyr Trp Arg Ala Tyr Ser Thr Asn Leu Leu Ser Ala
565 570 575

Glu Phe Leu Lys Gln Val Gln Ser His Leu Thr Pro Asp Gly Ile Val
580 585 590

Met Phe Asn Thr Thr His Ser Pro His Ala Phe Ala Thr Ala Val His
595 600 605

Ser Ile Pro Tyr Ala Tyr Arg Tyr Gly His Met Val Val Gly Ser Ala
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Thr Pro Val Val Phe Pro Asn Lys Glu Leu Leu Lys Gln Arg Leu Ser
625 630 635 640

Arg Leu Ile Trp Pro Glu Ser Gly Arg His Val Phe Asp Ser Ser Thr
645 650 655

Val Asp Ala Ala Ala Gln Lys Val Val Ser Arg Met Leu Ile Arg Met
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